

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 7.28571 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGQCSQNEYFDSLHACIP.....LTCQRYCNASVTNSVKGTNA 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	100.0	184	2	S43486
2	74.5	26.2	1101	2	T16840
3	70.5	24.8	1548	2	S34583
4	69.5	24.5	5376	2	T42215
5	66	23.2	63	2	S07127
6	66	23.2	330	2	T25169
7	65.5	23.1	1299	2	T43251
8	62.5	22.0	999	2	T19275
9	62.5	22.0	1513	2	T23691
10	61.5	21.7	483	2	S60231
11	61.5	21.7	483	2	T24856
12	61.5	21.7	520	2	G88846
13	60.5	21.3	1574	2	T13954
14	60.5	21.3	3034	2	T14119
15	59	20.8	758	2	T15577
16	59	20.8	1717	1	A45558
17	58.5	20.6	2533	3	T28675
18	58.5	20.6	2533	3	T28675
19	58	20.4	1816	1	S68960
20	57.5	20.2	1680	2	T43434
21	57	20.1	802	2	T20150
22	57	20.1	653	2	S36675
23	57	20.1	838	2	T20125
24	56.5	19.9	701	2	S62460
25	56	19.7	447	2	A96639
26	56	19.7	2476	2	T34022
27	56	19.7	2824	2	T22759
28	55.5	19.5	339	1	KHRTB
29	55.5	19.5	388	2	T31887

30	55.5	19.5	388	2	T31888
31	55.5	19.5	438	2	T31889
32	55.5	19.5	445	2	T31898
33	55.5	19.5	815	1	T05754
34	55.5	19.5	989	2	T01519
35	55	19.4	294	2	T23682
36	55	19.4	339	1	KHMSB
37	55	19.4	474	2	T27297
38	55	19.4	552	2	T27424
39	55	19.4	758	2	S46625
40	55	19.4	1620	2	T27283
41	54.5	19.2	392	2	T27303
42	54.5	19.2	419	2	S69207
43	54.5	19.2	493	2	JC5486
44	54.5	19.2	592	1	JC1480
45	54.5	19.2	2155	2	T30197

ALIGNMENTS

RESULT 1

S43486 B-cell maturation factor - human
N:Alternate names: BCM protein; BCMA protein; BEL protein
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C:Accession: S43486; S31208; S36661
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Teapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A:Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectional
A:Reference number: S43486; MUID:94218235; PMID:8165126
A:Accession: S43486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <LAA>
A:Cross-references: EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:9471245
R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Teapis, A.
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31208
A:Molecule type: mRNA
A:Residues: 1-184 <LA2>
A:Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:G29408
A:Accession: S36661
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-184 <LA3>
A:Cross-references: EMBL:Z14955
C:Genetics:
A:Gene: GDB:BCMA
A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Introns: 44/1; 93/1
C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 284; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.3e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKGTNA 51
|||||
DB 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKGTNA 54

RESULT 2

T16840
hypothetical protein T10810.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16840
R:Geisel, C.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid T10E10.

A:Reference number: 218598

A:Accession: T16840

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <GB1>

A:Cross-references: EMBL:U39644; NID:G1049339; PID:G1049343; PIDN:AAA80360.1; CESP:T10E10

A:Experimental source: Strain Bristol N2

C:Genetics:

A:Gene: CESP:T10E10.4

A:introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match 26.2%; Score 74.5; DB 2; Length 1101;

Best Local Similarity 36.7%; Pred. No. 1.2; Mismatches 15; Indels 5; Gaps 3;

Matches 18; Conservative 11; Mismatches 15; Indels 5; Gaps 3;

OY 4 QCSQNEVFDLSLHACIPQQLR--CSSNTPPLTCQRYCNASVTNSVKGTN 50

DB 350 QCSQSTVFNSDLNVCVPLAIONSCDSSTIQQVCS--C-SQVSSSCPGTS 395

RESULT 3

S34583

serine proteinase (EC 3.4.21.-) PC6B - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S34583

R:Nakagawa, T.; Murakami, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993

A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a

A:Reference number: S34583; MUID:93327934; PMID:8335106

A:Accession: S34583

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1548 <NAK>

A:Cross-references: GB:D17583; NID:G407344; PIDN:BA04507.1; PID:dl005033; PID:G440374

C:Keywords: hydrolase; serine proteinase

Query Match 24.8%; Score 70.5; DB 2; Length 1548;

Best Local Similarity 34.7%; Pred. No. 4.4; Mismatches 22; Indels 5; Gaps 1;

Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

OY 4 QCSQNEVFDLSLHACIPQQLR--CSSNTP--LTCQRYCNASVTNSVK 47

DB 1151 ECAAYEVNDEGSHRCQPHKRCSCGSPDQCTCPREPLNLTTCVK 1199

RESULT 4

T42215

zonadhesin - mouse

N:Alternate names: sperm-specific membrane protein

C:Species: Mus musculus (house mouse)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T42215

R:Gao, Z.; Garbers, D.L.

J. Biol. Chem. 273, 3415-3421, 1998

A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro

A:Reference number: 222080; MUID:98123114; PMID:9452463

A:Accession: T42215

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-5376 <GAO>

A:Cross-references: EMBL:U97068; NID:G3327420; PID:G3327421; PIDN:AAC26680.1

C:Genetics:

A:Gene: Zan

A:Map position: 5

C:Function: functions in multiple cell adhesion processes

A:Note: found exclusively on the apical region of the sperm head

C:Keywords: cell adhesion

Query Match 24.5%; Score 69.5; DB 2; Length 5376;

Best Local Similarity 36.8%; Pred. No. 16;

Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

OY 4 QCSQNEVFDLSLHACIP-QQLRCSNTP--PLTCQRYC 38

DB 3299 QCEPTNSQFTDCLPSCVSPSCNRCVTSPSVPSCHREGC 3336

RESULT 5

S07127

chymotrypsin/elastase inhibitor - common roundworm

C:Species: Ascaris lumbricoles (common roundworm)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S07127

R:Babin, D.R.; Peanasky, R.J.; Goos, S.M.

Arch. Biochem. Biophys. 232, 143-161, 1984

A:Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoles: the prim

A:Reference number: S07127; MUID:84255715; PMID:6564898

A:Accession: S07127

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-63 <BAB>

C:Superfamily: roundworm trypsin inhibitor

Query Match 23.2%; Score 66; DB 2; Length 63;

Best Local Similarity 34.0%; Pred. No. 0.93; Mismatches 18; Indels 8; Gaps 4;

Matches 17; Conservative 7; Mismatches 18; Indels 8; Gaps 4;

OY 5 QCSQNEVFDLSLHACIPQQLR--SSNTP-PLTCQRYCNASVTNSVKGTN 50

DB 5 CGNEVWTE---CTCEMKCGPDENTPCPLMCRPSCESGRGWRRTN 50

RESULT 6

T25169

hypothetical protein T23F1.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T25169

R:Wilkinson, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19990

A:Accession: T25169

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-330 <WIL>

A:Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6

C:Experimental source: clone T23F1

A:Gene: CESP:T23F1.6

A:Map position: 5

A:introns: 16/3

C:Superfamily: gliadin

Query Match 23.2%; Score 66; DB 2; Length 330;

Best Local Similarity 28.3%; Pred. No. 3.8; Mismatches 22; Indels 8; Gaps 2;

Matches 15; Conservative 8; Mismatches 22; Indels 8; Gaps 2;

OY 5 QCSQNEVFDLSLHACIP-----COLRCSNTPPL--TCQRYCNASVTNSVKGT 49

DB 59 CASSQOYQLOTSCQWPAQCOOSQOQOSNTNTQCOPTCOOSQOTSCNPMST 111

RESULT 7

T43251

furin (EC 3.4.21.75) - fall armyworm

N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; seri

C:Species: Spodoptera frugiperda (fall armyworm)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T43251

R:Chaplik, M.; Klenk, H.

submitted to the EMBL Data Library, January 1996

A:Description: Cloning and functional characterization of FURIN from Spodoptera frugiper

A;Reference number: Z2368
A;Accession: T43251
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1299 <CIE>
A;Cross-references: EMBL:Z68888; NID:gl167859; PID:e219690; PIDN:CAA93116.1
A;Experimental source: clone Sfurin 6; ovary
C;Function:
C;Description: responsible for the endoproteolytic processing of proproteins with specific keywords: hydrolase; serine proteinase

Query Match 23.1%; Score 65.5; DB 2; Length 1299;
Best Local Similarity 34.0%; Pred. No. 14;
Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

QY 5 CSQNEYFDSLHACIPQLRCS-----SNTPLTCQRYCNAS-----VTNSVKG 48
DB 1150 CSRPLRIDRLNNQVPC---CSERGVTNSTPTDC-CHCNPENGCINSSVAG 1198

RESULT 8
T19275
Hypothetical protein F34D10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T19275; T21723
R;Harris, B.
A;Reference number: Z19099
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Accession: T19275
A;Molecule type: DNA
A;Residues: 1-999 <WIL>
A;Cross-references: EMBL:Z37139; PIDN:CAA85494.1; GSPDB:GN00021; CESP:F34D10.2
A;Experimental source: clone C14B1
R;Kershaw, J.
Submitted to the EMBL Data Library, June 1994
A;Reference number: Z19464
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Accession: T21723
A;Molecule type: DNA
A;Residues: 1-999 <W12>
A;Cross-references: EMBL:Z34799; PIDN:CAA84320.1; GSPDB:GN00021; CESP:F34D10.2
A;Experimental source: clone F34D10
C;Genetics:
A;Gene: CESP:F34D10.2
A;Map position: 3
A;Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870

Query Match 22.0%; Score 62.5; DB 2; Length 999;
Best Local Similarity 42.5%; Pred. No. 24;
Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY 10 YFDSLHACIPQLRCSNTPLTCQRYCNASVTNSVKG 48
DB 516 YEDSLKTCIGRAFRVKKMTPLRIQYFVSSTPGLDG 555

RESULT 9
T23681
Hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23681
R;Matthews, L.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19781
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Accession: T23681
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Cross-references: EMBL:Z81573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M02G9.1
A;Experimental source: clone M02G9

C;Genetics:
A;Gene: CESP:M02G9.1
A;Map position: 2
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match 22.0%; Score 62.5; DB 2; Length 1513;
Best Local Similarity 35.8%; Pred. No. 34;
Matches 19; Conservative 3; Mismatches 18; Indels 13; Gaps 3;

QY 12 DSLHAC-IPCQLRCS-SNTPLTCQRYCNASV-----TNSVKG 51
DB 141 DSCNVQNVQGVSONSPAPVCOQTCRQSCQFGCATNEQLPTTSSSTNA 193

RESULT 10
S60231
Gibberellin-regulated protein GAS3 precursor - Arabidopsis thaliana
N;Alternate names: CAST1 protein homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 24-Sep-1999
C;Accession: S60231
R;Heizog, M.; Dorne, A.M.; Grellet, F.
Plant Mol. Biol. 27: 743-752, 1995
A;Title: GAS3, a gibberellin-regulated gene family from Arabidopsis thaliana related to F;1-18/Domain: signal sequence #status predicted <SIG>
A;Reference number: S60229; MUID:95244835; PMID:7727751
A;Accession: S60231
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99 <HER>
A;Cross-references: EMBL:U11764; NID:G887934; PIDN:AAB06308.1; PID:G887935
C;Genetics:
A;Gene: GAS3
C;Superfamily: gibberellin-regulated protein GAS2
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-99/Product: gibberellin-regulated protein GAS3 #status predicted <MAT>

Query Match 21.7%; Score 61.5; DB 2; Length 99;
Best Local Similarity 35.6%; Pred. No. 4.4;
Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;

QY 3 GQCSNEYFDSLHACIPQLRCSNTPLTCQRY---CNASVT 43
DB 47 GRCSKSRPNLCRLACNSCCYRCNC-VPECTAGNHHLCPCYASIT 90

RESULT 11
T24856
Hypothetical protein T12A7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24856
R;Lennard, N.
Submitted to the EMBL Data Library, June 1996
A;Reference number: Z19943
A;Accession: T24856
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-483 <WIL>
A;Cross-references: EMBL:Z73911; PIDN:CAA98142.2; GSPDB:GN00022; CESP:T12A7.2
A;Experimental source: clone T12A7
C;Genetics:
A;Gene: CESP:T12A7.2
A;Map position: 4
A;Introns: 36/3; 71/1; 146/1; 255/2; 287/2; 340/3; 387/1; 449/2

Query Match 21.7%; Score 61.5; DB 2; Length 483;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

QY 5 CSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVTNSVKG 48
DB 108 CMNDGYFNHTLGRGV-----CTSNWVGEHCIFRCNSGVWNTSG 146

RESULT 12

G88846
 protein T12A7.2 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: G88846
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see webistes genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: G88846
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-520<STO>
 A:Cross-references: GB:chr_IV; PIDN:CA98142.1; PID:G3879789; GSPDB:GN00022; CESP:T12A7.
 C:Genetics:
 A:Gene: T12A7.2
 A:Map position: 4

Query Match 21.7%; Score 61.5; DB 2; Length 520;
 Best Local Similarity 31.8%; Pred. No. 18;
 Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

OY 5 CSQNEVFDLHACIPQCLGSSNTPLTCQRCNASTVSVG 48
 DB 145 GANDGFNHTLGRV-----CTSNVGEHCIFRCNSGVNKTSG 183

RESULT 13

T13954
 MEGF6 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: T13954
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9693030
 A:Accession: T13954
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1574 <NAK>
 A:Cross-references: EMBL:AB011532; NID:G3449293; PIDN:BA032462.1; PID:G3449294
 A:Experimental source: strain Sprague-Dawley; brain
 C:Genetics:
 A:Gene: MEGF6

Query Match 21.3%; Score 60.5; DB 2; Length 1574;
 Best Local Similarity 32.2%; Pred. No. 59;
 Matches 19; Conservative 8; Mismatches 19; Indels 13; Gaps 4;

OY 2 AGQCSQNEVFDLHACIPQCL-----RCSSNTPLT---CORVC--NASVTNSVYG 48
 DB 963 ACNCSAGAPCDVAVTGSLT-CPAGRWGPRCAOSCPILTFGLNCSQITCFNGASCDVYG 1020

RESULT 14

T14119
 seven-pass transmembrane receptor protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14119
 R:Hadjilovakakis, A.K.; Formstone, C.J.; Little, P.F.R.
 submitted to the EMBL Data Library, October 1997
 A:Description: The Celar family of novel evolutionarily conserved seven-pass transmembrane
 A:Reference number: Z17881
 A:Accession: T14119
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-3034 <HAD>

A:Cross-references: EMBL:AF031572; NID:G3800735; PID:G3800736; PIDN:AAC68836.1

C:Genetics:
 A:Gene: Celar1
 A:Map position: 15
 C:Keywords: transmembrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>

Query Match 21.3%; Score 60.5; DB 2; Length 3034;
 Best Local Similarity 28.3%; Pred. No. 1e+02;
 Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;

OY 4 QCSQNEVFDLHACIPQCL-----RCSSNTPLTQ-----RYCN-----ASVTN 44
 DB 2001 QCKENYKPPADACLPCDPCFHGSHSRACMDTQGCACKRGVIGRCNRCNDNPFAYTS 2060

RESULT 15

T15577
 hypothetical protein C23G10.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
 C:Accession: T15577
 R:Latreille, P.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C23G10.
 A:Reference number: Z18372
 A:Accession: T15577
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-758 <LAT>
 A:Cross-references: EMBL:U39851; NID:G1055062; PID:G1055068; PIDN:AAA81069.1; CESP:C23G
 C:Genetics:
 A:Gene: CESP:C23G10.8
 A:introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8

Query Match 20.8%; Score 59; DB 2; Length 758;
 Best Local Similarity 42.9%; Pred. No. 47;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 12 DSLHACIPQCLGSSNTPL 32
 DB 260 ESVFPHLYPABIRCSADGPPL 280

Search completed: January 7, 2003, 09:41:06
 Job time : 9.28572 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:39 ; Search time 12.1855 Seconds
(without alignment)
371.797 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201

Sequence: 1 CSQNEYFSLHACIPQLRCSNTPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 101002.*

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2:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	34	AAE15486	Human B-cell matur
2	201	100.0	51	AAE15485	Human B-cell matur
3	201	100.0	58	AAE15501	Human B-cell matur
4	201	100.0	181	AAE15484	Human B-cell matur
5	201	100.0	184	AAE15483	Amino acid sequenc
6	201	100.0	184	AAE15482	A human BCMA prote
7	201	100.0	184	AAE15481	Human BCMA protein
8	201	100.0	184	AAE15480	Human B-cell matur
9	201	100.0	184	AAE15479	Human B-cell matur
10	201	100.0	184	AAE15478	Human B-cell matur

11	201	100.0	184	ABB81487	Human BCMA recepto
12	201	100.0	283	AAE15488	Human BCMA-immunog
13	201	100.0	302	AAE00507	Human BCMA-immunog
14	201	100.0	302	AAE00509	Mouse IGG signal/h
15	159.5	79.4	157	AAE00700	Human BAPF recepto
16	136	67.7	185	AAE08844	Amino acid sequenc
17	136	67.7	185	AAE071980	Murine B cell matur
18	136	67.7	185	AAE15490	Mouse B cell matur
19	93.5	46.5	117	AAE15489	Human-murine B cel
20	90.5	45.0	24	AAE15491	Human-murine BCMA
21	71.5	35.6	249	AAE15492	A murine ztnf4, a
22	66.5	33.1	33	AAE15493	Human TACI cystein
23	66.5	33.1	37	AAE15494	Human AGP-3 recept
24	66.5	33.1	37	AAE15495	Human TACI cystein
25	66.5	33.1	59	AAE15500	Human lymphocyte s
26	66.5	33.1	166	AAE15496	Human TACI extrace
27	66.5	33.1	166	AAE15497	Human TACI splice
28	66.5	33.1	291	AAE15498	Human AGP-3 recept
29	66.5	33.1	293	AAE15499	Human lymphocyte s
30	66.5	33.1	293	AAE15500	Human neutrokin-a
31	66.5	33.1	293	AAE15501	A transmembrane ac
32	66.5	33.1	293	AAE15502	Human TACI protein
33	66.5	33.1	293	AAE15503	Human tumour necro
34	66.5	33.1	293	AAE15504	Human TACI-IgG Ec
35	66.5	33.1	293	AAE15505	Human TACI recepto
36	66.5	33.1	293	AAE15506	Human transmembran
37	66.5	33.1	293	AAE15507	Tumour necrosis fa
38	66.5	33.1	293	AAE15508	Human transmembran
39	66.5	33.1	293	AAE15509	Human AGP-3 relate
40	66.5	33.1	312	AAE15510	Protein of N-termi
41	66.5	33.1	334	AAE15511	Protein of hTACI (
42	66.5	33.1	366	AAE15512	Protein of hTACI (
43	66.5	33.1	397	AAE15513	Human TACI-immunog
44	66.5	33.1	404	AAE15514	Protein of a compl
45	66.5	33.1			

ALIGNMENTS

RESULT 1

AAE15486

ID AAE15486 standard; peptide; 34 AA.

XX AAE15486;

XX AAE15486;

DT 12-MAR-2002 (first entry)

XX Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US15567.

XX 12-MAY-2000; 2000US-204039P.

XX 27-JUN-2000; 2000US-214591P.

XX 14-MAY-2001; 2001US-0214591.

XX (AMGE-) AMGEN INC.

XX

PI The11 LE, Yu G;
XX
XX WPI; 2002-066686/09.
DR
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PI family ligand
XX
XX
PS Claim 1; Fig 10A; 94p; English.

XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein cysteine-rich consensus region.

SQ Sequence 34 AA;

Query Match 100.0%; Score 201; DB 23; Length 34;
Best Local Similarity 100.0%; Pred. No. 7,4e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYC 34
DB 1 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYC 34

RESULT 2

ID AAE15485 standard; peptide; 51 AA.

XX AAE15485;

DT 12-MAR-2002 (first entry)

DE Human B-cell maturation (BCMA) protein extracellular domain.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytochrome B cell maturation protein; BCMA; tumor necrosis factor-TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

PR 14-MAY-2001; 2001US-0214591.

PA (AMGE-) AMGEN INC.
XX
XX The11 LE, Yu G;
XX
XX WPI; 2002-066686/09.
DR
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PI family ligand
XX
XX
PS Claim 1; Fig 10A; 94p; English.

XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein extracellular domain.

SQ Sequence 51 AA;

Query Match 100.0%; Score 201; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYC 34
DB 5 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYC 38

RESULT 3

ID AAE15501 standard; peptide; 58 AA.

XX AAE15501;

DT 12-MAR-2002 (first entry)

DE Human B cell maturation protein cysteine rich extracellular region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytochrome B cell maturation protein; BCMA; tumor necrosis factor-TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

```

PR 14-MAY-2001; 2001US-0214591.
PA (AMGE-) AMGEN INC.
XX Theill LE, Yu G;
PI WPI; 2002-066686/09.
DR Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX Disclosure; Fig 13; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA cysteine-rich extracellular region.
XX
XX Sequence 58 AA;
XX
XX Query Match 100.0%; Score 201; DB 23; Length 58;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-18;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34
XX ||||||||||||||||||||||||||||||||||
XX Db 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34
XX
XX RESULT 4
XX AAEL15484
XX ID AAEL15484 standard; Protein; 181 AA.
XX
XX AC AAEL15484;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Human B-cell maturation (BCMA) protein.
XX
XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX
XX Region 5..38
XX /note= "Cysteine-rich consensus region; This is region
XX is specifically claimed as SEQ ID NO: 7 in claim 1 of
XX the specification"
XX 52..72
XX
XX Domain

```

```

ET /label= Transmembrane_domain
XX WO200187979-A2.
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand
XX
XX Disclosure; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein.
XX
XX Sequence 181 AA;
XX
XX Query Match 100.0%; Score 201; DB 23; Length 181;
XX Best Local Similarity 100.0%; Pred. No. 4e-18;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34
XX ||||||||||||||||||||||||||||||||||
XX Db 5 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 38
XX
XX RESULT 5
XX AAB08843
XX ID AAB08843 standard; peptide; 184 AA.
XX
XX AC AAB08843;
XX
XX DT 02-JAN-2001 (first entry)
XX
XX DE Amino acid sequence of human.
XX
XX KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
XX anti-cell death gene; apoptosis; viral infection; inflammatory response;
XX rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers

```

FT Domain 57..77 /note= "putative transmembrane domain"
XX
XX
XX WO2000050633-A1.
XX
XX 31-AUG-2000.
XX
XX
XX 24-FEB-2000; 2000WO-US04925.
XX
XX 24-FEB-1999; 99US-0121485.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX
XX Seed B, Ting A;
XX
XX WPI; 2000-558405/51.
XX
XX
XX Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
XX gene and reporter gene, and determining alteration in reporter gene
XX expression -
XX
XX Claim 32; Fig 7A; 53pp; English.
XX
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA
XX is a necrosis factor (NF)-KB activator. The method of the invention is
XX used to identify compounds which modulate BCMA activity (and thus NF-KB
XX activity). The specification describes a method of identifying a
XX polypeptide which increases gene expression from a promoter. The method
XX involves contacting a library of with a cell which expresses a
XX recombinant anti-cell death gene and a reporter gene operably linked to
XX the promoter, and then determining whether the expression of the
XX reporter gene is altered as a result of contact with library. The method
XX is useful for identifying polypeptides which increase or decrease gene
XX expression from a promoter. The BCMA polypeptide or nucleic acid are
XX useful for preparing a pharmaceutical composition for treating cancer,
XX apoptosis, viral infections, inflammatory response, such as rheumatoid
XX arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
XX identifying compounds that modulate NF-KB expression and thus for drug
XX designing.
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 201; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 4,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 34
DB 8 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 41
RESULT 6
AAE094001
ID AAE094001 standard; Protein; 184 AA.
XX
XX AAE094001;
XX
XX 20-OCT-2000 (first entry)
XX
XX A human BCMA protein, a B cell protein related to TACI.
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX znf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; neuropathy;
XX renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.

XX
XX Homo sapiens.
XX
XX WO200040716-A2.
XX
XX 13-JUL-2000.
XX
XX
XX 07-JAN-2000; 2000WO-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
XX (ZIMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX
XX WPI; 2000-452538/39.
XX
XX N-PSDB; AAA58559.
XX
XX
XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX
XX Disclosure; Page 152; 175pp; English.
XX
XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX domain of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for
XX inhibiting znf4 activity. A znf4 is a TNF ligand, they may also be used
XX for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
XX with activating BR43x2, TACI or BCMA receptor-ligand engagement associated
XX with activated or resting B lymphocytes, effector T-cells, or with
XX autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
XX and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
XX asthma, bronchitis, emphysema, nephritis, pyelonephritis, renal
XX glomerulonephritis, vasculitis, end stage renal failure,
XX neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
XX amyloidosis, moderating immune response, immunosuppression, graft
XX rejection, graft versus host disease, inflammation, insulin dependent
XX diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
XX septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
XX agonists or antagonists can be used to treat hypertension, renal artery
XX stenosis, or occlusion, and cholesterol or renal emboli.
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 201; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 4,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 34
DB 8 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 41
RESULT 7
AAE09241
ID AAE09241 standard; Protein; 184 AA.
XX
XX AAE09241;
XX
XX 19-NOV-2001 (first entry)
XX
XX Human BCMA protein.
XX
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
XX TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis;
XX psoriasis.
XX
XX Homo sapiens.
OS

XX WO200160397-A1.
 XX 23-AUG-2001.
 XX 28-NOV-2000; 2000WO-US32378.
 XX 16-FEB-2000; 2000US-0182938.
 XX 22-AUG-2000; 2000US-0226986.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 XX Yan M;
 XX WPI; 2001-541628/60.
 XX N-PSDB; AAD15902.
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 XX activity, for treating autoimmune disorders and cancer, comprises
 XX exposing the cells to TALL-1 or APRIL polypeptide agonists or
 XX antagonists -
 XX Example 2; Fig 2; 160pp; English.
 XX The invention relates to methods of using one or more agonists or
 XX antagonists to modulate the activity of the members of TNF (tumour
 XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 XX e.g. TACI or BCMA. The method is useful for treating pathological
 XX conditions or diseases associated with increased TALL-1 and APRIL
 XX expression or activity. TALL-1 and APRIL antagonists are used to
 XX block the interaction between APRIL and TALL-1 with TACI or BCMA.
 XX They are useful for treating a mammal suffering from cancer such
 XX as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 XX autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 XX psoriasis and lupus erythematosus. The present sequence is human
 XX BCMA protein.
 XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQLRCSNTPTLCQRYC 34
 |||||
 Db 8 CSONEYFDSLHACIPQLRCSNTPTLCQRYC 41

RESULT 8
 AAE00506
 ID AAE00506 standard; Protein; 184 AA.
 XX AC
 XX AAE00506;
 XX 31-JUL-2001 (first entry)
 XX Human B cell maturation protein (BCMA).

XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 XX organ transplantation; HIV; human immunodeficiency virus; TNF;
 XX tumour necrosis factor; BCMA; B cell maturation protein.
 XX Homo sapiens.
 XX WO200124811-A1.
 XX 12-APR-2001.

PF 05-OCT-2000; 2000WO-US27579.
 XX 06-OCT-1999; 99US-0157933.
 PR 11-FEB-2000; 2000US-0181807.
 PR 30-JUN-2000; 2000US-0215888.
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
 XX WPI; 2001-266242/27.
 DR N-PSDB; AAD03844.

XX Treating a mammal for a condition associated with undesired cell
 XX proliferation such as cancer or carcinoma, comprises administering a
 XX composition comprising A Proliferation Inducing Ligand Receptor
 XX (APRIL-R) antagonist -
 XX Claim 3; Fig 3A; 85pp; English.

XX The invention relates to a method of treating a mammal for a condition
 XX associated with undesired cell proliferation such as cancer or
 XX carcinoma. The method involves administering a composition comprising
 XX A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
 XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the
 XX interaction between APRIL and its cognate receptor(s). This method is
 XX useful for treating undesired cell proliferation such as cancer or
 XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 XX prostate carcinoma and other carcinomas whose proliferation is modulated
 XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
 XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 XX diseases, renal disorders, B-cell lympho-proliferative disorders,
 XX immunosuppressive diseases, organ transplantation, inflammation and
 XX human immunodeficiency virus (HIV) and for treating, suppressing or
 XX altering an immune response involving a signalling pathway between
 XX APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 XX The present sequence is human APRIL-R also referred as BCMA or
 XX BCM protein.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQLRCSNTPTLCQRYC 34
 |||||
 Db 8 CSONEYFDSLHACIPQLRCSNTPTLCQRYC 41

RESULT 9
 AAB60698
 ID AAB60698 standard; Protein; 184 AA.
 XX AC
 XX AAB60698;
 XX 22-MAY-2001 (first entry)
 XX Human BAPF receptor (BAPF-R).

XX Human BAPF-R; BAPF receptor; TNF family; immunoregulatory agent;
 XX immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;
 XX B-cell maturation inhibitor; immunoglobulin production disorder; HIV infection;
 XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 XX renal disorder; immunosuppressive disorder; HIV infection;
 XX organ transplantation; antiinflammatory; systemic lupus erythematosus;
 XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 XX lymphoma; gene therapy; cancer; tumour.
 XX Homo sapiens.

PN WO200112812-A2.
 XX 22-FEB-2001.
 PD 16-AUG-2000; 2000WO-US22507.
 PF 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX
 PA (BIOI) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P,
 PI Thompson J;
 XX WPI; 2001-202866/20.
 DR N-PSDB; AAF59998.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAF-R-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAF-R
 PT antibody homolog -
 XX
 XX Claim 20; Fig 1; 59pp; English.
 XX
 CC The invention relates to the use of a BAF-R receptor (BAF-R, also known
 CC as BCMA) protein, or a BAF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hyperendosin and
 CC related disorders. BAF-R, fusion proteins containing it, and BAF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders. B-cell lymphoproliferative
 CC disorders, hyperendosin and renal disorders. The BAF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAF-R
 CC proteins or BAF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAF-R and BAF-R, thereby inhibiting inflammation. Since BAF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinoma, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAF-R.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-16;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEVFDLSLHACIPQQLRCSSTNPPLTCQRYC 34
 DB 8 CSQNEVFDLSLHACIPQQLRCSSTNPPLTCQRYC 41
 XX
 RESULT 10
 ID AAY71979 standard; Protein; 184 AA.
 XX
 AC AAY71979;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Human B cell maturation factor (BCMA) protein.
 XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

KM systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KM thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KM haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KM post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KM B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Domain 1..62
 FT /label= Extracellular_domain
 XX
 EN WO200068378-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12266.
 XX
 PR 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Shu HS;
 XX
 DR WPI; 2001-016094/02.
 DR N-PSDB; AAD02125.
 XX
 PT Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 XX Claim 37; Page 104-105; 112pp; English.
 XX
 CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC
 CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16, in human tissues. BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEVFDLSLHACIPQQLRCSSTNPPLTCQRYC 34
 DB 8 CSQNEVFDLSLHACIPQQLRCSSTNPPLTCQRYC 41
 XX
 RESULT 11
 ID ABB81487 standard; Protein; 184 AA.
 XX

AC ABB81487;
 DT 02-SEP-2002 (first entry)
 XX Human BCMA receptor related protein SEQ ID NO:7.
 DE
 XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiaschematic;
 KW nephroprotective; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; nephritis;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; amyloidosis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; large vessel disease;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200238766-A2.
 XX
 PD 16-MAY-2002.
 XX
 XX 05-NOV-2001; 2001WO-US47018.
 XX
 XX 07-NOV-2000; 2000US-246449P.
 XX
 XX 20-DEC-2000; 2000US-257131P.
 XX
 XX 28-JUN-2001; 2001US-201715P.
 XX
 XX 29-AUG-2001; 2001US-315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 PI WPI; 2002-508212/54.
 XX
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 XX Disclosure; Page 135-136; 154pp; English.
 PS
 CC The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiaschematic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 23; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CSQNEYFDSLHACIPQCLACSSNTPTLCQRYC 34

DB 8 CSQNEYFDSLHACIPQCLACSSNTPTLCQRYC 41
 RESULT 12
 AAE15488
 ID AAE15488 standard; Protein; 283 AA.
 XX
 AC AAE15488;
 DT 12-MAR-2002 (first entry)
 XX
 XX Human BCMA-immunoglobulin Fc region fusion protein.
 DE
 XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US15567.
 XX
 XX 12-MAY-2000; 2000US-204039P.
 XX
 XX 27-JUN-2000; 2000US-214531P.
 XX
 XX 14-MAY-2001; 2001US-0214591.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Theill LE, Yu G;
 PI WPI; 2002-066686/09.
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 XX
 XX Disclosure; Fig 10B; 94pp; English.
 PS
 CC The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70 a tumour necrosis factor-TNF
 CC family ligand) having the consensus sequence of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein-immunoglobulin Fc region fusion protein.
 XX
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 201; DB 23; Length 283;
 Best Local Similarity 100.0%; Pred. No. 6.3e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYC 34
 DB 5 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYC 38

RESULT 13

AAE0507
 ID AAE0507 standard; Protein; 302 AA.

AC AAE0507;

DT 31-JUL-2001 (first entry)

DE Human BCMA-Immunoglobulin G Fc region fusion construct.

XX Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
 KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
 KW immunoglobulin G; IgG; Fc region.

OS Chimeric - Homo sapiens.

XX Chimeric - Mus sp.

FH Key Location/Qualifiers

FT 1..22 /label= Signal peptide

FT /note= "Derived from murine Ig kappa sequence"

FT /label= Mature_human_BCMA_IgG_Fc_fusion_protein

FT 23..75 /note= "Derived from human BCMA protein"

FT Region /note= "Derived from human IgG Fc region"

FT Domain /label= Cysteine-rich domain

FT /note= "Derived from human BCMA"

XX WO200124811-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27579.

XX 06-OCT-1999; 99US-0157933.

XX 11-FEB-2000; 2000US-0181807.

XX 30-JUN-2000; 2000US-0215688.

XX (BIOJ) BIOGEN INC.

XX (APOT-) APOTEC R & D SA.

XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;

XX WPI, 2001-266242/27.

XX N-PSDB; AAD03847.

XX Treating a mammal for a condition associated with undesired cell

XX proliferation such as cancer or carcinoma, comprising administering a

XX composition comprising a Proliferation Inducing Ligand Receptor

XX (APRIL-R) antagonist.

XX Example 1; Fig 3B; 85pp; English.

CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and
 CC human immunodeficiency virus (HIV); and for treating, suppressing or
 CC altering an immune response involving a signalling pathway between
 CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 CC The present sequence is a fusion construct containing human APRIL-R
 CC also referred as BCMA or BCM protein, Fc region of human immunoglobulin
 CC G (IgG) and a signal sequence from murine Ig kappa cDNA.

XX Sequence 302 AA;

SQ Query Match 100.0%; Score 201; DB 22; Length 302;

Best Local Similarity 100.0%; Pred. No. 6.8e-18;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYC 34

DB 31 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYC 64

RESULT 14

AAE0699
 ID AAE0699 standard; Protein; 302 AA.

AC AAE0699;

DT 22-MAY-2001 (first entry)

DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.

XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.

XX Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX WO200112812-A2.

XX 22-FEB-2001.

XX 16-AUG-2000; 2000WO-US22507.

XX 17-AUG-1999; 99US-0149378.

XX 11-FEB-2000; 2000US-0181684.

XX 18-FEB-2000; 2000US-0183536.

XX (BIOJ) BIOGEN INC.

XX (APOT-) APOTEC R & D SA.

XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P,

XX Thompson J;

XX WPI, 2001-202866/20.

XX N-PSDB; AAF59999.

XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell

XX lympho-proliferative disorder by administering BAFF-receptor

XX polypeptide, chimeric molecule comprising receptor or anti-BAFF-R

XX antibody homolog -

XX Example 4; Fig 2; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFF-R fusion protein BAFF-R-Fc,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153
 CC of human BAFF-R and a human IgG Fc sequence.

XX Sequence 302 AA;

Query Match 100.0%; Score 201; DB 22; Length 302;
 Best Local Similarity 100.0%; Pred. No. 6.6e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCQRCSNTPTLCQRYC 34
 DB 31 CSQNEYFDSLHACIPQCQRCSNTPTLCQRYC 64

RESULT 15

AAB60700

ID AAB60700 standard; Protein; 157 AA.

AC AAB60700;

DT 22-MAY-2001 (first entry)

DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.

KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;
 KW B-cell maturation inhibitor; B-cell lymphoproliferative disorder; hypertension;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; HIV infection;
 KW renal disorder; immunosuppressive disorder; organ transplantation;
 KW organ transplantation; antinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.

OS Homo sapiens.

PN WO200112812-A2.

PD 22-FEB-2001.

PF 16-AUG-2000; 2000WO-US22507.

PR 17-AUG-1999; 99US-0149378.

PR 11-FEB-2000; 2000US-0181684.

PR 18-FEB-2000; 2000US-0183536.

PA (BIOJ) BIOGEN INC.

PA (APOT-) APOTEC R & D SA.

PI MacKay F, Browning J, Ambrose C, Tschopp J, Schneider P;

PI Thompson J;
 XX WPI: 2001-202866/20.
 DR N-PSDB; AAF60000.

XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
 PT antibody homolog -

PS Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents a human BAFF-R protein sequence as encoded
 CC by plasmid pJST535. However, this BAFF-R protein sequence is 27 amino
 CC acids shorter than that given in AAB60698.

XX Sequence 157 AA;

Query Match 79.4%; Score 159.5; DB 22; Length 157;
 Best Local Similarity 90.6%; Pred. NO. 7.4e-13;
 Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 QNEYFDSLHACIPQCQRCSNTPTLCQRYC 34

DB 7 QNEYFDSLHACIPQCQLR---NTPPLTCQRYC 35

Search completed: January 7, 2003, 09:37:26
 Job time : 13:1855 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 4.85714 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201
Sequence: 1 CSQNEYPDSLHACIPQLRCSSNTPLTCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	201	100.0	184	2 S43486	B-cell maturation factor
2	67.5	33.6	1548	2 S34583	serine proteinase
3	64.5	32.1	5376	2 T42215	zonadhesin - mouse
4	61	30.3	1101	2 T16840	hypothetical prote
5	59	29.4	758	2 T15577	hypothetical prote
6	58	28.9	1299	2 T43251	furin (EC 3.4.21.7
7	57.5	28.6	63	2 S07127	chymotrypsin/elast
8	57.5	28.6	1680	2 A43434	furin (EC 3.4.21.7
9	57	28.4	1717	1 A45558	epidermal growth f
10	56	27.9	2476	2 T34022	zonadhesin - pig
11	55.5	27.6	989	2 T01519	hypothetical prote
12	55	27.4	330	2 T25169	hypothetical prote
13	55	27.4	1513	2 T23681	hypothetical prote
14	54.5	27.1	2155	2 T30197	alpha tectorin - m
15	54	26.9	1980	2 S4307	myosin heavy chain
16	54	26.9	2022	2 A32256	myosin-Ixb (sialin
17	53.5	26.6	758	2 S46625	finger protein YJL
18	53	26.4	1574	2 T13954	MSGF6 protein - ra
19	53	26.4	2824	2 T22759	hypothetical prote
20	52.5	26.1	118	2 S61051	hypothetical prote
21	52	25.9	255	2 A84544	hypothetical prote
22	52	25.9	294	2 T23682	hypothetical prote
23	52	25.9	547	2 T34318	hypothetical prote
24	52	25.9	1474	2 D88550	protein ZC84.6 lim
25	52	25.9	2844	2 S28291	hypothetical prote
26	51.5	25.6	63	2 S57816	antimicrobial pept
27	51.5	25.6	282	2 S35754	siab-1B protein -
28	51.5	25.6	282	2 I48763	siab-1A protein -
29	51.5	25.6	497	2 T27827	hypothetical prote

30	51.5	25.6	915	2 T21773	hypothetical prote
31	51.5	25.6	927	2 T21772	hypothetical prote
32	51.5	25.6	999	2 T19275	hypothetical prote
33	51.5	25.6	2120	2 T30243	alpha tectorin - c
34	51	25.4	641	2 E96612	probable transcrip
35	51	25.4	653	2 G96675	hypothetical prote
36	51	25.4	746	2 G84605	hypothetical prote
37	50.5	25.1	610	1 I46001	C4b-binding protei
38	50	24.9	63	2 S08572	chymotrypsin/elast
39	50	24.9	74	2 S10332	ubiquitin / riboso
40	50	24.9	342	2 T30370	hypothetical prote
41	50	24.9	376	2 C81272	probable aminotran
42	50	24.9	455	1 G0HUT1	tumor necrosis fac
43	50	24.9	561	2 T27318	hypothetical prote
44	50	24.9	626	2 T27319	hypothetical prote
45	50	24.9	922	2 T23573	hypothetical prote

ALIGNMENTS

RESULT 1

S43486
B-cell maturation factor - human
N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: S43486; S31208; S36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire
A;Reference number: S43486; MUID:94218235; PMID:8165126
A;Accession: S43486
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z29574; NID:G471244; PIDN:CAA82690.1; PID:G471245
EMBO J. 11, 3897-3904, 1992
R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;1
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z14954; NID:G29407; PIDN:CAA78679.1; PID:G29408
A;Accession: S36661
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 4-184 <LA3>
A;Cross-references: EMBL:Z14955
C;Genetics:
A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 201; DB 2; Length 184;

Best Local Similarity 100.0%; Pred No. 2,7e-17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

QY 1 CSQNEYPDSLHACIPQLRCSSNTPLTCQRYC 34

DB 8 CSQNEYPDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 2

S34583

serine proteinase (EC 3.4.21.-) PC6B - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C;Accession: S34583

R;Nakagawa, T.; Murakami, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:D17583; NID:9407344; PIDN:BA04507.1; PID:d1005033; PID:g440374
C:Keywords: hydrolase; serine proteinase

Query Match 33.6%; Score 67.5; DB 2; Length 1548;
Best Local Similarity 37.8%; Pred. No. 2.3;
Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCSNTPP-----LTCOR 32
DB 1152 CAVEYWDGSHRCQPCCHKKCRSGSPSEDQCTCPR 1188

RESULT 3
T42215
zonadhesin - mouse
N:Alternate names: sperm-specific membrane protein
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T42215
J:Gao, Z.; Garbers, D.L. 1998
J. Biol. Chem. 273, 3415-3421, 1998
A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro
A:Reference number: 222080; MUID:98123114; PMID:9452463
A:Accession: T42215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5376 <GAO>
A:Cross-references: EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:MAC26680.1
C:Genetics:
A:Gene: Zan
A:Map position: 5
C:Function:
A:Description: functions in multiple cell adhesion processes
A:Note: found exclusively on the apical region of the sperm head
C:Keywords: cell adhesion

Query Match 32.1%; Score 64.5; DB 2; Length 5376;
Best Local Similarity 35.1%; Pred. No. 16;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 1 CSONEYFDSLHACIPCOLRCSNTPP-----PLTCOR 34
DB 3300 CPTNSQFTDCLPSCVPSNRCVTSVPSSCREGC 3336

RESULT 4
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16840
R:Geisel, C.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 30.3%; Score 61; DB 2; Length 1101;

Best Local Similarity 37.5%; Pred. No. 11;
Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCSNTPPPLTC 30
DB 351 CSQTVFNSDLNVCVPLAIONSCDSSTQOPVC 382

RESULT 5
T15577
hypothetical protein C23G10.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T15577
R:Latreille, P.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C23G10.
A:Reference number: Z18372
A:Accession: T15577
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-758 <LAT>
A:Cross-references: EMBL:U39851; NID:g1055062; PID:g1055068; PIDN:AAA81069.1; CESP:C23G
A:Gene: CESP:C23G10.8
A:Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8

Query Match 29.4%; Score 59; DB 2; Length 758;
Best Local Similarity 42.9%; Pred. No. 14;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 8 DSLHACIPCOLRCSNTPPL 28
DB 260 BSVFPLYPARICSGADGPPL 280

RESULT 6
T43251
furin (RC 3.4.21.75) - fall armyworm
N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; seri
C:Species: Spodoptera frugiperda (fall armyworm)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43251
R:Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A:Description: Cloning and functional characterization of FURIN from Spodoptera frugipe
A:Reference number: Z22368
A:Accession: T43251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1299 <CIE>
A:Cross-references: EMBL:Z6888; NID:g167859; PID:e219690; PIDN:CAA93116.1
A:Experimental source: clone Sfurin 6; ovary
C:Function:
A:Description: responsible for the endoproteolytic processing of proproteins with speci
C:Keywords: hydrolase; serine proteinase

Query Match 28.9%; Score 58; DB 2; Length 1299;
Best Local Similarity 37.1%; Pred. No. 28;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps 2;

QY 1 CSONEYFDSLHACIPCOLRCS-----SNTPPLTC 30
DB 1150 CSRPLRIDRLNQCVCPC---CSERGYNSTPTPTC 1181

RESULT 7
S07127
chymotrypsin/elastase inhibitor - common roundworm
C:Species: Ascaris lumbricoides (common roundworm)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S07127

R:Babin, D.R.; Pearsley, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A:Title: The inhibitors of chymotrypsin/elastase from *Ascaris lumbricoides*: the prima
A:Reference number: S07127; MUID:84255715; PMID:6564898
A:Accession: S07127

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <BAB>
C:Superfamily: roundworm trypsin inhibitor

Query Match 28.6%; Score 57.5; DB 2; Length 63;
Best Local Similarity 37.1%; Pred. No. 2.5;
Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

QY 1 CSONEYFDSLHACIPCOLRCS--SSNTP-PLTCQR 32
DB 5 CGPNEVWTE---CTGCEMKCGPDENTPCPLMCRR 35

RESULT 8

A43434
furin (EC 3.4.21.75) 2 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROB>
A:Cross-references: GB:M94375; NID:gl57461; PID:gl57462
A:Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBI:P:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Cross-references: FlyBase:FBgn0004598
C:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 28.6%; Score 57.5; DB 2; Length 1680;
Best Local Similarity 34.3%; Pred. No. 41;
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCS-NTPPLTCQRYC 34
DB 1199 CSESEFYQVQGRPCPCASCGSCNGPACTCTCTSC 1233

RESULT 9

A45558
epidermal growth factor receptor homolog precursor - fluke (*Schistosoma mansoni*)
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: *Schistosoma mansoni*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A45558; S27836
R:Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A:Title: Alternative splicing of the *Schistosoma mansoni* gene encoding a homologue of ep
A:Reference number: A45558; MUID:92365727; PMID:1501637
A:Accession: A45558
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1717 <SHO>
A:Cross-references: EMBL:M86396; NID:gl60957; PIDN:AAA29866.1; PID:gl60958
A:Note: sequence extracted from NCBI backbone (NCBI:P:111129)
C:Genetics:
A:Gene: SER

C:Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F:1018-1323/Domain: protein kinase homology <KIN>
F:1026-1034/Region: protein kinase ATP-binding motif

Query Match 28.4%; Score 57; DB 1; Length 1717;
Best Local Similarity 40.9%; Pred. No. 48;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCS 22
DB 646 CPRNTYIDPQTRHCLPCNCS 667

RESULT 10

T34022
zonadhesin - pig
C:Species: *Sus scrofa domestica* (domestic pig)
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T34022
R:Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A:Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
A:Reference number: Z21464; MUID:96064658; PMID:7592795
A:Accession: T34022
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2476 <HAR>
A:Cross-references: EMBL:U40024; NID:gl066465; PID:gl066466; PIDN:AAC48486.1
A:Experimental source: strain Meishan; testis
C:Genetics:
A:Gene: Zan
C:Function:
A:Description: may be involved in sperm adhesion to the zona pellucida

Query Match 27.9%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 86;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSONEYFDSLHACIP-CQ--LRCSNTPPLTCQRYC 34
DB 1851 CSAHSVTVCSCLPSCQDPGQCTGAGAPSTCEGC 1888

RESULT 11

T01519
hypothetical protein T10M13.17.1 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01519
R:Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
Martienssen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997

A:Description: The sequence of the *Arabidopsis thaliana* T10M13 BAC.
A:Reference number: Z14346
A:Accession: T01519
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-989 <JOH>
A:Cross-references: EMBL:AF001308; NID:gl2104523; PID:g3912931
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4S
A:Introns: 31/3
A:Note: T10M13.17.1

Query Match 27.6%; Score 55.5; DB 2; Length 989;
Best Local Similarity 41.9%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 10; Indels 5; Gaps 2;

QY 1 CSONEYFDSLHACIPC-----QURCSNTPPP 27
DB 540 CARN-IDRLFLYHCSPCNFTDLRLCVLNPPPP 569

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RESULT 12
T25169
hypothetical protein T23F1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25169
R:Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19990
A:Accession: T25169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-330 <MIL>
A:Cross-references: EMBL:Z81129; PIDN:CA803405.1; GSPDB:GN00023; CESP:T23F1.6
A:Experimental source: clone T23F1
C:Genetics:
A:Gene: CESP:T23F1.6
A:Map position: 5
A:introns: 16/3
C:Superfamily: gliadin

Query Match
Best Local Similarity 27.4%; Score 55; DB 2; Length 330;
Matches 12; Conservative 28.6%; Pred. No. 20;
Mismatches 15; Indels 8; Gaps 2;

QY 1 CSQNEYPDSLHACIP-----COLRCSNTPPLTCORYC 34
DB 59 CASSQOYLOTSCMCAACSCSCQCCSNTNTPCPTCCQSC 100

RESULT 13
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23681
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19781
A:Accession: T23681
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1513 <MIL>
A:Cross-references: EMBL:Z81573; PIDN:CA804625.1; GSPDB:GN00020; CESP:M02G9.1
A:Experimental source: clone M02G9
C:Genetics:
A:Gene: CESP:M02G9.1
A:Map position: 2
A:introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match
Best Local Similarity 27.4%; Score 55; DB 2; Length 1513;
Matches 13; Conservative 44.8%; Pred. No. 74;
Mismatches 11; Indels 2; Gaps 2;

QY 8 DSLHAC-IPCOLRC-SSNTPPLTCORYC 34
DB 141 DSCQNCVNCVCGACVSONSPPAVCOQTC 169

RESULT 14
T30197
alpha tectorin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T30197
R:legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.
J. Biol. Chem. 272, 8791-8801, 1997
A:Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to corn
A:Reference number: Z20771; PMID:97236843; PMID:9079715
A:Accession: T30197
A:Status: preliminary; translated from GB/EMBL/DBJ
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A:Molecule type: mRNA
A:Residues: 1-2155 <LECG>
A:Cross-references: EMBL:X99805; NID:G1915908; PIDN:CAA68138.1; PID:G1915909
A:Experimental source: strain CD1; whole cochlea
A>Note: non-collagenous protein only expressed in the inner ear, by cells both in and s

Query Match
Best Local Similarity 27.1%; Score 54.5; DB 2; Length 2155;
Matches 10; Conservative 29.4%; Pred. No. 1.2e+02;
Mismatches 15; Indels 3; Gaps 1;

QY 1 CSQNEYPDSLHACIPCOLRCSNTPPLTCORYC 34
DB 1372 CPPNSHYSCVSCVCP--RCALRLKSDCNHYC 1402

RESULT 15
S54307
myosin heavy chain - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C:Accession: S54307
R:Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A:Title: A novel type of myosin implicated in signalling by rho family GTPases.
A:Reference number: S54307; PMID:95188874; PMID:7882973
A:Accession: S54307
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1980 <REL>
A:Cross-references: EMBL:X72609; NID:G639998; PIDN:CAA54700.1; PID:G639999
C:Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C
C:Keywords: nucleotide binding; P-loop
F:143-942/Domain: myosin motor domain homology <MNOT>
F:139-246/Region: nucleotide-binding motif A (P-loop)
F:1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match
Best Local Similarity 26.9%; Score 54; DB 2; Length 1980;
Matches 9; Conservative 52.9%; Pred. No. 1.2e+02;
Mismatches 2; Indels 0; Gaps 0;

QY 16 PCOLRCSNTPPLTCOR 32
DB 1812 PCLLRCPDPSDPLTSMK 1828

Search completed: January 7, 2003, 09:41:08
Job time : 6.85714 secs
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 2.55639 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201

Sequence: 1 CSQNEYFDSLHLHACIPQLRCSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	184	1	TR17_HUMAN
2	136	67.7	185	1	TR17_MOUSE
3	71.5	35.6	249	1	T13X_MOUSE
4	67.5	33.6	1877	1	PCRS_MOUSE
5	66.5	33.1	293	1	T13X_HUMAN
6	64.5	32.1	5376	1	ZAN_MOUSE
7	60	29.9	867	1	SSPO_BOVIN
8	58	28.9	175	1	T13C_MOUSE
9	57.5	28.6	63	1	ICB1_ASCSU
10	57.5	28.6	1680	1	FUR2_DROME
11	56	27.9	2476	1	YAN_FIG
12	55	27.4	708	1	YB40_HUMAN
13	54	26.9	1980	1	MY9B_RAT
14	54	26.9	2114	1	MY9B_MOUSE
15	54	26.9	2158	1	MY3B_HUMAN
16	53.5	26.6	381	1	P53_CANFA
17	53.5	26.6	758	1	YU6 YEAST
18	53	26.4	131	1	ALK1_MOUSE
19	52.5	26.1	1592	1	SORL1_CHICK
20	51.5	25.6	63	1	AME2_MIRJA
21	50.5	25.1	610	1	CAEP_BOVIN
22	50.5	25.1	1013	1	PRML_DROME
23	50	24.9	72	1	RL40_TOBAC
24	50	24.9	455	1	TRIA_HUMAN
25	50	24.9	1696	1	PCK5_BRACL
26	49	24.4	297	1	XEDA_HUMAN
27	49	24.4	321	1	MEC3_CAEEL
28	49	24.4	350	1	PAX4_HUMAN
29	49	24.4	461	1	TRIA_FIG
30	49	24.4	1483	1	UFPA YEAST
31	49	24.4	1984	1	YL_DROME
32	49	24.4	2531	1	NTC1_MOUSE
33	49	24.4	3718	1	LMA5_MOUSE

34	48.5	24.1	323	1	TNR6_BOVIN
35	48.5	24.1	608	1	ALB1_SALSA
36	48.5	24.1	608	1	ALB2_SALSA
37	48.5	24.1	3034	1	CLRI_MOUSE
38	48	23.9	56	1	ITR4_RADMA
39	48	23.9	304	1	TFPI_MACMU
40	48	23.9	448	1	EDAF_HUMAN
41	48	23.9	450	1	RMIL_AVEVR
42	48	23.9	500	1	SAH2_HUMAN
43	48	23.9	515	1	APX1_CAEEL
44	48	23.9	611	1	SAH3_HUMAN
45	48	23.9	681	1	COG2_CAEEL

PS1867 bos taurus
P21848 salmo salar
O03156 salmo salar
O35161 mus musculus
P16344 radianthus
Q28864 macaca mula
Q9960 homo sapien
P27966 avian tous
O43858 homo sapien
P41950 caenorhabdi
Q96nm2 homo sapien
Q21444 caenorhabdi

ALIGNMENTS

RESULT 1

TR17_HUMAN

ID TR17_HUMAN STANDARD; PRT; 184 AA.

AC Q02223;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).

DE TNFRSF17 OR BCMA OR BCM.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. AND CHROMOSOMAL TRANSLOCATION.

RC ISSUES=Peripheral blood leukocytes, and Lymph node;

RX MEDLINE=93010984; PubMed=1396583;

RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;

RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";

RL EMBO J. 11:3897-3904(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=94218235; PubMed=8165126;

RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;

RT "The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";

RL Nucleic Acids Res. 22:1147-1154(1994).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=9425270; PubMed=10493829;

RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush P., Brandon R., Fuhrmann J., Mason T., Sroebv M.L., Barnstead M., Cronin L., Deallates Mays A., Cao X., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;

RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";

RL Genomics 60:295-308(1999).

RN [4]

RP SEQUENCE FROM N.A. AND VARIANT THR-153.

RX MEDLINE=21419161; PubMed=11528522;

RA Kawasaki A., Teuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;

RT "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";

RL Genes Immun. 2:276-279(2001).

RN [5]

RP FUNCTION.

RX MEDLINE=20363816; PubMed=10903733;

RA Hatzoglu A., Rousset J., Bourgeade M.-F., Rogier E., Madry C., Inoue J., Devergne O., Tsapis A.;

RT "TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38

RT J. Immunol. 165:1322-1330(2000).
 [6]
 RP FUNCTION.
 RA MEDLINE=20259066; PubMed=10801128; Enselman R., Dillon S.R.,
 RA Gross J.A., Johnston J., Mudri S., Foster D., Lofton-Day C.,
 RA Madden K., Xu W., Parrish-Novak J., Postor D., Lofton-Day C.,
 RA Moore M., Litzau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clagett C.H., Theil L.E.,
 RT "APRIL and TALL-1 are receptors for a TNF homologue implicated in B-cell
 RT autoimmunity disease." Nature 404:995-999(2000).
 RL Nature 404:995-999(2000).
 RN (7)
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RA MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theil L.E.,
 RT "APRIL and TALL-1 are receptors for a TNF homologue implicated in B-cell
 RT humoral immunity." Nat. Immunol. 1:252-256(2000).
 RL Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RA MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.,
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1." Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16) (Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC
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 CC -----
 DR EMBL: Z14954; CAAT7679.1; -
 DR EMBL: Z29575; CAAG2691.1; -
 DR EMBL: Z29574; CAAG2690.1; -
 DR EMBL: U95747; AAB67251.1; -
 DR EMBL: AB052772; BAB60895.1; -
 DR PIR: S31208; S31208.
 DR PIR: S31209; S31209.
 DR Gene; HGNC:11913; TNFRSF17.
 DR MIM: 109545; -
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal extracellular; Polymorphism.
 FT DOMAIN 1 54
 FT TRANSMEM 55 77
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT TNFR-CYS.
 FT REPEAT 7 41
 FT SITE 3 4
 FT INTERLEUKIN 2/BCM ONCOGENE.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT VARIANT 153 153
 FT A -> T.
 FT /FTID=VAR_012234.
 FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D32 CRC64;

Query Match 100.0%; Score 201; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.8e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CSONEYPDSILHACIPCOLRCSNTPPLTCORYC 34
 DB 8 CSONEYPDSILHACIPCOLRCSNTPPLTCORYC 41
 RESULT 2
 ID TR1_MOUSE STANDARD; PRT; 185 AA.
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFSF17 OR BCM4 OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BAUB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
 RT "The characterization of murine BCM4 gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily." J.
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peele G., Quackenbush J.,
 RA Schmitt L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weir C., Whitaker C., Wilming L.,
 RA Watanabe-Borja A., Yoshida K., Hasegawa Y., Kawaji H., Kontseki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection." J.
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC
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DR EMBL; AF061505; AAC23799.1; -;
 DR EMBL; AK020247; BAB32038.1; -;
 DR MGD; MGI:1343050; Tnfref17.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KW Alternative splicing.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 71 185 TNFR-CYS.
 FT REPEAT 4 36 BY SIMILARITY.
 FT DISULFID 5 18 BY SIMILARITY.
 FT DISULFID 21 32 BY SIMILARITY.
 FT DISULFID 25 36 BY SIMILARITY.
 FT VARSPLIC 87 91 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 67.7%; Score 136; DB 1; Length 185;
 Best Local Similarity 70.6%; Pred. No. 1e-10; 6; Indels 2; Gaps 1;
 Matches 24; Conservative 2; Mismatches 6;

QY 1 CSQNEYFDSLLHACIPCOLRCSSTNPTPLTCQRYC 34
 DB 5 CPHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36

RESULT 3

TI3X MOUSE STANDARD; PRT; 249 AA.
 AC Q9ET35; Q9DBZ3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFSF13B OR TACI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=21177254; PubMed=1081172;
 RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 RA Dixit V.M.;
 RA "Identification of a receptor for BLYS demonstrates a crucial role in
 RA humoral immunity.";
 RL Nat. Immunol. 1:37-41 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai K., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo T., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
 RA Blake K., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10890535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovyev I., Lee P., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Hsu H.;
 RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:137-143 (2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TACI-ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice.";
 RL Nat. Immunol. 2:632-637 (2001).
 CC -I- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC -I- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLG with its C-terminus (by similarity).
 CC -I- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -I- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -----
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EMBL; AF257673; BAB22457.1; -;
 EMBL; AK004668; BAB22457.1; -;
 MGD; MGI:1889411; Tnfref13b.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS0050; TNFR_NGFR_2; 2.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 5 38 TNFR-CYS 1.
 FT REPEAT 42 76 TNFR-CYS 2.
 FT DISULFID 6 19 BY SIMILARITY.
 FT DISULFID 22 34 BY SIMILARITY.
 FT DISULFID 26 38 BY SIMILARITY.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 65 76 BY SIMILARITY.
 FT CONFLICT 137 137 I -> F (IN REF. 2).
 SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;
 Query Match 35.6%; Score 71.5; DB 1; Length 249;
 Best Local Similarity 35.3%; Pred. No. 0.025; 13; Indels 1; Gaps 1;
 Matches 12; Conservative 8; Mismatches 13;

QY 1 CSQNEYFDSLLHACIPCOLRCSSTNPTPLTCQRYC 34

DB 6 CPKDQYDSSRKSCVSCALTCQSORS-ORTCTDFC 38

RESULT 4

PCK5 MOUSE STANDARD; PRT; 1877 AA.
 ID _PCK5_MOUSE

AC 004592; 062040; (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 41, last annotation update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Proprotein convertase PCS) (Subtilisin/kexin-like protease PCS)
 DE (Convertase PCS) (Pcs) (Subtilisin-like proprotein convertase 6)
 DE (SPC6).
 GN PCS6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
 RC STRAIN=ICR; TISSUE=Intestine;
 RX MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RL J. Biochem. 113:132-135(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=9342056; PubMed=8341687;
 RA Lussan J., Vileau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "CDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [4]
 RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RX MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RT Bendayan M., Seidah N.G.;
 RL "The isoforms of proprotein convertase PCS are sorted to different
 subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275(1996).
 RN [5]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=96293359; PubMed=8698813;
 RA Constant D.B., Calton M., Robertson E.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 RN [6]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-VAL-1-ZAA BONDS, WHERE XAA
 CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO

CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 CC EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, PCSB/LONG (SHOWN HERE)
 CC AND PCSA/SHORT, ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 CC ABUNDANT IN THE TESTIS AND ADRENALS. PCSB IS EXPRESSED IN THE
 CC TESTIS, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 CC EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE LIVER AND THE LUNG,
 CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 CC E6.5, PROMINENT EXPRESSION OBSERVED IN EXTRAEMBRYONIC ENDODERM, ANION AND
 CC NASCENT MESODERM. AT E8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
 CC SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT BETWEEN
 CC E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
 CC CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
 CC TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
 CC STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
 CC CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
 CC ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
 CC ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
 CC ISOFORM B OCCUR AT E12.5.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 CC SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 CC WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
 CC -----
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 CC AT THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
 CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
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 CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE <http://www.isb-sib.ch/announce/>
 CC OR SEND AN EMAIL TO license@sib-sib.ch).
 CC -----
 CC EMBL: D17583; BA04507.1; -
 CC EMBL: D12619; BA02143.1; -
 CC EMBL: L14932; AA74636.1; -
 CC PIR: JX0248; JX0248.
 CC PIR: A48225; A48225.
 CC HSPG: O99405; IMPT.
 CC MEROPS: S08.076; -.
 CC MGD: MGI:97515; PcsK5.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR002174; Furin-like.
 CC InterPro: IPR002884; P domain.
 CC InterPro: IPR002029; Peptidase_S8.
 CC Pfam: PF00082; Peptidase_S8; 1.
 CC Pfam: PF01483; P-partial.
 CC PRINTS: PR00723; SUBTILISIN.
 CC PRODOM: PD000717; P-domain; 1.
 CC SMART: SM00181; EGF_3.
 CC SMART: SM00001; EGF-like; 2.
 CC SMART: SM00261; FU; 22.
 CC PROSITE: PS00136; SUBTILASE ASP; 1.
 CC PROSITE: PS00137; SUBTILASE HIS; 1.
 CC PROSITE: PS00138; SUBTILASE SER; 1.
 CC Hydrolase: Serine protease; Glycoprotein; Zymogen; Signal;
 CC Cleavage on pair of basic residues; Repeat; Alternative splicing;
 CC Transmembrane.
 CC SIGNAL 1 34
 CC PROPEP 35 116
 CC CHAIN 117 1877
 CC DOMAIN 117 1768
 CC TRANSMEM 1769 1789
 CC DOMAIN 1790 1877
 CC DOMAIN 117 452
 CC DOMAIN 464 602
 CC HOMO B.
 CC PROTEIN CONVERTASE SUBTILISIN/KEXIN
 CC TYPE 5.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC CATALYTIC.
 CC HOMO B.

[illegible]

Query Match 32.1%; Score 64.5; DB 1; Length 5376;
 Best Local Similarity 35.1%; Pred. No. 3.3; Mismatches 3; Gaps 2;
 Matches 13; Conservative 5;
 QY 1 CSONEYFDSLLHACIP-COLRCSSNTP--PLTCQRYC 34
 DB 3300 CPTNSQFTCLFSCVSCNRCVTPSPVSSCRGEC 3336

RESULT 7
 SSPO_BOVIN
 ID SSPO_BOVIN STANDARD; PRT; 867 AA.
 AC P98167;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE SCO-spondin (Fragment)
 OS Bos taurus (Bovine)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ependymocyte;
 RX MEDLINE=96338614; PubMed=8743952;
 RA Gobron S., Monnerie H., Meinert R., Creveaux I., Lehmann W.,
 RA Lamalle D., Dastugue B., Meinert A.;
 RA "SCO-spondin: a new member of the thrombospondin family secreted by
 RT the subcommissural organ is a candidate in the modulation of neuronal
 RT aggregation.";
 RL J. Cell Sci. 109:1053-1061(1996).
 CC -!- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
 CC -!- DEVELOPMENTAL STAGE: EMBRYO.
 CC -!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
 CC -!- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
 CC -!- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
 CC -!- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
 CC -!- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
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 CC -----
 CC EMBL; X93922; CAA63815.1; -;
 CC HSP; P01130; IAUJ.
 CC InterPro; IPR000421; FAS8 C.
 CC InterPro; IPR002172; LDL_recept_A.
 CC InterPro; IPR002919; TIL_Cysrich.
 CC InterPro; IPR000884; TSF1.
 CC InterPro; IPR001007; VWF C.
 CC Pfam; PF00057; ldl_recept_a; 3.
 CC Pfam; PF00093; vwc; 1.
 CC Pfam; PF00754; vwf; 4.
 CC Pfam; PF01826; TIL; 1.
 CC SMART; SM00231; FAS8C; 1.
 CC SMART; SM00192; LDLA; 3.
 CC SMART; SM00209; TSF1; 4.
 CC SMART; SM00214; VWC; 1.
 CC PROSITE; PS01285; FAS8C_1; 1.
 CC PROSITE; PS01286; FAS8C_2; 1.
 CC PROSITE; PS01209; LDLA_1; 3.
 CC PROSITE; PS01209; LDLA_2; 3.
 CC PROSITE; PS00688; LDLA_2; 3.
 CC PROSITE; PS00692; TSF1; 4.
 CC Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
 KW NON_TER

FT DOMAIN 26 81 TSP TYPE-1 1.
 FT DOMAIN 103 142 EGF-LIKE 1.
 FT DOMAIN 143 180 EGF-LIKE 2.
 FT DOMAIN 185 243 TSP TYPE-1 2.
 FT DOMAIN 344 502 F5/8 TYPE C.
 FT DOMAIN 506 544 LDL-RECEPTOR CLASS A 1.
 FT DOMAIN 663 701 LDL-RECEPTOR CLASS A 2.
 FT DOMAIN 723 761 LDL-RECEPTOR CLASS A 3.
 FT DOMAIN 762 813 TSP TYPE-1 3.
 FT DOMAIN 814 867 TSP TYPE-1 4.
 FT DISULFID 107 122 BY SIMILARITY.
 FT DISULFID 116 127 BY SIMILARITY.
 FT DISULFID 129 141 BY SIMILARITY.
 FT DISULFID 147 166 BY SIMILARITY.
 FT DISULFID 149 169 BY SIMILARITY.
 FT DISULFID 171 179 BY SIMILARITY.
 FT DISULFID 344 502 BY SIMILARITY.
 FT DISULFID 508 520 BY SIMILARITY.
 FT DISULFID 515 533 BY SIMILARITY.
 FT DISULFID 527 542 BY SIMILARITY.
 FT DISULFID 665 677 BY SIMILARITY.
 FT DISULFID 672 690 BY SIMILARITY.
 FT DISULFID 684 699 BY SIMILARITY.
 FT DISULFID 725 737 BY SIMILARITY.
 FT DISULFID 732 750 BY SIMILARITY.
 FT DISULFID 744 759 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT NON_TER 867 867
 SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;
 Query Match 29.9%; Score 60; DB 1; Length 867;
 Best Local Similarity 42.9%; Pred. No. 2.3;
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
 QY 10 LLHACIPCOLRCSSNTPPLTC 30
 DB 96 VFHACVCPCLTCDDISQATC 116

RESULT 8
 T13C_MOUSE
 ID T13C_MOUSE STANDARD; PRT; 175 AA.
 AC Q9D8D0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE tumor necrosis factor receptor superfamily member 13C (B cell-
 DE activating factor receptor) (BAFF receptor) (BAFF-R) (BlyS receptor
 DE 3) (B-cell maturation defect).
 DE TNFRSF13C OR BAFFR OR BCMD OR BR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
 RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.;
 RA "BAFF-R, a newly identified TNF receptor that specifically interacts
 RT with BAFF.";
 RL Science 293:2108-2111(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
 RC STRAIN=A/J;
 RX MEDLINE=21475520; PubMed=11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
 RA Cancro M.P., Grewal I.S., Dixit V.M.;

RT "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";
 RT Curr. Biol. 11:1547-1552(2001).
 RN [3]

RP SOURCE FROM N.A. (ISOPORN 1).
 RC STRAIN-G57BL/6J; TISSUE-Small intestine;
 RX MEDLINE=21085660; PubMed=11217651;

RA Kawai Y., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Komio H., Adachi J., Fukuda S.,
 RA Atzawa K., Ozawa M., Nishi K., Kiyosawa H., Kondo S., Yamahara I.,
 RA Saito T., Kazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseuk S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RN [4]

RP FUNCTION

RA MEDLINE=21614654; PubMed=11747827;
 RA Harless S.M., Lenz V.M., San A.P., Hsu B.L., Clise-Dwyer K.,
 RA Hilbert D.M., Hayes C.E., Cancro M.P.;
 RT Competition for Blyc-mediated signaling through Bcnd/BR3 regulates
 RT peripheral B lymphocyte numbers.";
 RL Curr. Biol. 11:1986-1989(2001).
 CC - FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.
 CC - SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC - ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC - TISSUE SPECIFICITY: Highly expressed in spleen and testis;
 CC detected at lower levels in lung and thymus.
 CC - DISEASE: Defects in TNFSF13C are a cause of severe B-cell
 CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
 CC in the BAFF gene leading to an altered C-terminus. The mutant RNA
 CC is not detectable. B-cell lymphopoiesis is normal, but the life
 CC span of peripheral B-cells is much reduced.
 CC - SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.

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CC EMBL: AF373847; AAK91827.1; -;
 CC EMBL: AK008142; BAB25490.1; -;
 CC MGD: MGI:1919299; Tnfrsf13c.

KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 KW alternative splicing.

FT DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 92 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 21 38 TNFR-CYS (PARTIAL).
 FT DISULFID 22 35 BY SIMILARITY.
 FT DISULFID 27 38 BY SIMILARITY.
 FT CARBOHYD 23 35 N-LINKED (GLCNAC.) (POTENTIAL).
 FT VARSPLIC 133 143 MISSING (IN ISOPORN 2).
 SQ SEQUENCE 173 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 28.9%; Score 58; DB 1; Length 175;
 Best Local Similarity 47.4%; Pred. No. 0.95;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GSONEYFDSLHACIPCOL 19
 Db 22 CNGTECFDPLNVCVCEL 40

RESULT 9

ICEL_ASCSU STANDARD; PRT; 63 AA.
 AC P07851;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUL-1999 (Rel. 36, Last annotation update)
 DE Chymotrypsin/elastase isoform 1 (C/E-1 inhibitor).
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
 OC NCB1_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84255715; PubMed=6564898;
 RA Babin D.R., Peanasky R.J., Goos S.M.;
 RT "The isoforms of chymotrypsin/elastase from Ascaris
 RT lumbricoides: the primary structure.";
 RL Arch. Biochem. Biophys. 232:143-161(1984).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
 RX MEDLINE=95006335; PubMed=7922044;
 RA Huang K., Striyacka N.C., Bernard V.D., Peanasky R.J., James M.N.;
 RT "The molecular structure of the complex of Ascaris
 RT chymotrypsin/elastase inhibitor with porcine elastase.";
 RL Structure 2:679-689(1994).
 CC - FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.
 CC - SIMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.
 DR PIR: S07127; S07127.
 DR PDB: 1EAI; 05-APR-99.
 DR InterPro: IPR002919; TIL_Cysrich.
 KW pfam: PF01826; TIL; 1.
 KW Serine protease inhibitor; 3D-structure.
 FT DISULFID 5 38
 FT DISULFID 14 33
 FT DISULFID 17 29
 FT DISULFID 21 60
 FT DISULFID 40 54
 FT ACT SITE 31 32
 SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;

Query Match 28.6%; Score 57.5; DB 1; Length 63;
 Best Local Similarity 37.1%; Pred. No. 0.43;
 Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

Qy 1 GSONEYFDSLHACIPCOLRC--SSNP-PLTCOR 32
 Db 5 CGPNEVWTE---CTGCEMKCGPDENTPCPLMCCR 35

RESULT 10

PIR2_DROME STANDARD; PRT; 1680 AA.
 AC P30432;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
 GN FUR2.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Empidoidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

RN SEQUENCE FROM N.A. PubMed=1512259;
 RP MEDLINE=92381036; PubMed=1512259;
 RA Roebrock A.J.M., Cremers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
 Renkrop M., Gattef E.A.F., Leunissen J.A.M., van de Ven W.J.;
 RT Cloning and functional expression of Dfurlin2, a subtilisin-like
 RI protease and functional enzyme of Drosophila melanogaster with multiple
 RT repeats of a cysteine motif.;
 RL J. Biol. Chem. 267:17208-17215 (1992).
 CC -!- FUNCTION: FURLIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPROTEASE
 CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
 CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
 CC propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
 CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
 CC complement component C3 and von Willebrand factor from their
 CC respective precursors.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURLIN SUBFAMILY.
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 CC
 DR EMBL; W94375; AA28551.1; -.
 DR FIR; A43434; A43434.
 DR HSP; Q99405; IMPT.
 DR MEROPS; S08.049; -.
 DR FLYBASE; FGN0004598; Fur2.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002884; P domain.
 DR InterPro; IPR000209; Peptidase S8.
 DR Pfam; PF00082; Peptidase S8.
 DR Pfam; PF01483; P; PARTIAL.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P domain; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 DR Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane;
 KW Multigene family; Zymogen; Repeat.
 FT SIGNAL; 1; 2
 FT SIGNAL; 1; 2
 FT PROPEP 1 319
 FT CHAIN 320 1690
 FT ACT_SITE 418 418
 FT ACT_SITE 457 457
 FT ACT_SITE 638 638
 FT DOMAIN 962 1444
 FT REPEAT 962 1007
 FT REPEAT 1008 1057
 FT REPEAT 1058 1104
 FT REPEAT 1105 1153
 FT REPEAT 1154 1205
 FT REPEAT 1206 1254
 FT REPEAT 1255 1299
 FT REPEAT 1300 1346
 FT REPEAT 1347 1393
 FT REPEAT 1394 1444
 FT TRANSMEM 1508 1532
 FT DOMAIN 1533 1690
 FT CARBOHYD 3
 FT CARBOHYD 109 109
 FT CARBOHYD 130 130
 FT CARBOHYD 203 203
 FT CARBOHYD 443 443
 FT CARBOHYD 481 481
 FT CARBOHYD 928 928
 FT CARBOHYD 928 928

FT CARBOHYD 1061 1061 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1182 1182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1275 1275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1278 1278 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1440 1440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1680 AA; 183599 MW; 0A99CE8770A8E293 CRC64;
 Query Match 28.8%; Score 57.5; DB 1; Length 1680;
 Best Local Similarity 34.3%; Pred. No. 8.9; Indels 1; Gaps 1;
 Matches 12; Conservative 5; Mismatches 17;
 QY 1 CSQNEYFDSLHACIPQLRCSS-NTPPLTCQRYC 34
 Db 1199 CSESEFYQVEGQCRPCHASCSCGSPADTCTSC 1233
 RESULT 11
 ZAN_PIG STANDARD; PRT; 2476 AA.
 ID ZAN_PIG
 AC Q28983;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Zonadhesin precursor.
 GN ZAN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN
 RP SEQUENCE FROM N.A.; AND SEQUENCE OF 823-830; 859-872; 883-890;
 RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;
 RP 1658-1667; 1777-1795 AND 1914-1921.
 RC STRAIN=Meishan; TISSUE=Testis;
 RX MEDLINE=96064658; PubMed=7592795;
 RA Hardy D.M., Garbers D.L.;
 RT "A sperm membrane protein that binds in a species-specific manner to
 RT the egg extracellular matrix is homologous to von Willebrand
 RT factor.";
 RL J. Biol. Chem. 270:26025-26028 (1995).
 CC -!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
 CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
 CC SIGNALING.
 CC -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
 CC APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
 CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.
 CC -!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
 CC ZONA PELLUCIDA.
 CC -!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
 CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
 CC SPERMATOZOIA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
 CC -!- DOMAIN: THE WFED DOMAINS 2 AND 3 MAY MEDIATE COVALENT
 CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
 CC -!- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING
 CC FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
 CC PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
 CC CAPACITATION.
 CC -!- SIMILARITY: CONTAINS 2 MAM DOMAINS.
 CC -!- SIMILARITY: CONTAINS 4.5 WFED DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U40024; AAC48486.1; -.
 DR HSP; P56682; 1CCV.

DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000998; MAM domain.
DR InterPro; IPR002919; Tili-Cyrich.
DR InterPro; IPR003328; Tili-Cyrich.
DR InterPro; IPR001007; VME_C.
DR InterPro; IPR001846; VME_D.
DR Pfam; PF00094; VWD; 4.
DR Pfam; PF00629; MAM; 2.
DR Pfam; PF01826; TIL; 5.
DR Pfam; PF02345; TIL; 5.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00214; VWC; 2.
DR SMART; SM00216; VWD; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 2.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
Repeat.
KW Repeat.
FT SIGNAL 1 29
FT CHAIN 30 2476
FT DOMAIN 30 2418
FT TRANSMEM 2419 2439
FT TRANSMEM 2440 2476
FT DOMAIN 31 144
FT DOMAIN 147 312
FT DOMAIN 319 687
FT 688 789
FT DOMAIN 800 1184
FT 1185 1373
FT DOMAIN 1574 1968
FT DOMAIN 1969 2370
FT DOMAIN 2366 2402
FT DISULFID 2370 2381
FT DISULFID 2375 2390
FT DISULFID 2381 2401
FT CARBOHYD 109 109
FT CARBOHYD 269 269
FT CARBOHYD 735 735
FT CARBOHYD 758 758
FT CARBOHYD 833 833
FT CARBOHYD 833 833
FT CARBOHYD 1154 1154
FT CARBOHYD 1329 1329
FT CARBOHYD 1448 1448
FT CARBOHYD 1544 1544
FT CARBOHYD 1596 1596
FT CARBOHYD 1654 1654
FT CARBOHYD 1843 1843
FT CARBOHYD 1965 1965
FT CARBOHYD 2122 2122
FT CARBOHYD 2165 2165
FT CARBOHYD 2178 2178
FT CARBOHYD 2329 2329
FT CARBOHYD 2359 2359
FT CARBOHYD 823 823
FT CONFLICT 923 923
FT CONFLICT 965 965
FT CONFLICT 1241 1241
SQ SEQUENCE 2476 AA; 270364 MW; A13B590375A548C CRC64;

Query Match 27.9%; Score 56; DB 1; Length 2476;
Best Local Similarity 31.6%; Pred. No. 20;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSONEYFDSLHACIP-CQ---LRCSNRPPLTCQRYC 34
DB 1851 CSASHSVTSCVPCSLPSCQDPBEGCTGAGAPSTCEGC 1888
RESULT 12
YB40_HUMAN

ID YB40 HUMAN STANDARD; PRT; 708 AA.
AC Q9UT0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein KIAA1140 (Fragment).
GN KIAA1140;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain;
RC MEDLINE=20039618; PubMed=10574461;
RA Hirotsawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
CC -!- SIMILARITY: CONTAINS 8 TPR REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB012966; BAA6454.1; .
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 7.
DR SMART; SM00028; TPR; 3.
KW Hypothetical protein; Repeat; TPR repeat.
FT NON_TER 1
FT REPEAT 27 60 TPR 1.
FT REPEAT 264 297 TPR 2.
FT REPEAT 347 381 TPR 3.
FT REPEAT 383 415 TPR 4.
FT REPEAT 416 449 TPR 5.
FT REPEAT 495 528 TPR 6.
FT REPEAT 630 662 TPR 7.
FT REPEAT 663 696 TPR 8.
SQ SEQUENCE 708 AA; 79140 MW; 8B93440B522CFC1C CRC64;

Query Match 27.4%; Score 55; DB 1; Length 708;
Best Local Similarity 38.2%; Pred. No. 8.4;
Matches 13; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCSNRPPLTCQRYC 34
DB 277 CGKSAVAVSLRECV-KLRSDPTVPLMAKVC 308

RESULT 13
MY9B_RAT
ID MY9B_RAT STANDARD; PRT; 1980 AA.
AC Q6358;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mysin IXb (Unconventional myosin-9b).
GN MYO9B OR MYR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain stem, and Spinal cord;
RX MEDLINE=95188874; PubMed=7882973;
RA Reinhard J., Scheel A.A., Diekmann D., Hall A., Ruppert C.,

BAehler M.;
 RA "A novel type of myosin implicated in signalling by rho family
 RT GTPases";
 RL EMBL J. 14:697-704 (1995).
 CC -!- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
 CC ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.
 CC MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS
 CC ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP
 CC AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.
 CC ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON RHO.
 CC -!- SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLOCALIZES WITH
 CC F-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS
 CC LOCALIZATION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE
 CC PERINUCLEAR REGION (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, LUNG, THYMUS, BRAIN,
 CC LIVER, AND SPLEEN.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -!- SIMILARITY: CONTAINS 4 IQ DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X77609; CRA54700.1; -.
 CC HSSP; P08799; LMND.
 CC InterPro; IPR002219; DAG_PE_BIND.
 CC InterPro; IPR000048; IQ_region.
 CC InterPro; IPR000159; RA_domain.
 CC InterPro; IPR000198; RhGAP.
 CC InterPro; IPR001609; myosin_head.
 CC Pfam; PF00063; myosin_head; 2.
 CC Pfam; PF00130; DAG_PE_BIND; 1.
 CC Pfam; PF00612; IQ_4.
 CC Pfam; PF00620; RhGAP; 1.
 CC Pfam; PF00788; RA; 1.
 CC PRINTS; PR00193; MYOSINHEAVY.
 CC ProDom; PR000355; myosin_head; 2.
 CC SMART; SM00109; C1; 1.
 CC SMART; SM00242; MYSC; 1.
 CC SMART; SM00314; RA; 1.
 CC SMART; SM00324; RhGAP; 1.
 CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
 CC PROSITE; PS00096; IQ; 3.
 CC MYOSIN; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
 CC Cytoskeleton; Coiled coil; GTPase activation; Phorbol-ester binding;
 CC Zinc.
 CC FT DOMAIN 1 940 HEAD OR MOTOR DOMAIN.
 CC FT DOMAIN 941 1045 NECK OR REGULATORY DOMAIN.
 CC FT DOMAIN 1046 1380 TAIL.
 CC FT DOMAIN 1841 1861 COILED COIL (POTENTIAL).
 CC FT DOMAIN 1918 1948 COILED COIL (POTENTIAL).
 CC FT DOMAIN 845 856 ACTIN-BINDING.
 CC FT DOMAIN 958 978 IQ 1.
 CC FT DOMAIN 981 1001 IQ 2.
 CC FT DOMAIN 1002 1024 IQ 3.
 CC FT DOMAIN 1025 1054 IQ 4.
 CC FT DOMAIN 1593 1641 PHORBOL-ESTER AND DAG BINDING.
 CC FT DOMAIN 1673 1822 RHO-GAP.
 CC FT NP_BIND 239 246 ATP (POTENTIAL).
 CC SEQUENCE 1980 AA; 225035 MW; D79FEC4D0FAE0C05 CRC64;
 Query Match 26.9%; Score 54; DB 1; Length 1980;
 Best Local Similarity 52.9%; Pred. No. 29;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 PCOLRCSSNTPPLTCOR 32
 DB 1812 PCLLRCPDSDPLTSMK 1828
 RESULT 14
 MY9B MOUSE
 ID MY9B MOUSE STANDARD; PRT: 2114 AA.
 AC Q9QY06; Q9QY07; Q9QY08; Q9QY09;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin IXb (Unconventional myosin-9b).
 GN MYO9B OR MYR5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS.
 RC STRAIN=C57BL/6;
 RX MEDLINE=20047919; PubMed=10580159;
 RA Grewal P.K., Jones A.-W., Macnouchie M., Lemmers R.J.F., Frants R.R.,
 RA Hewitt J.E.;
 RT Cloning of the murine unconventional myosin gene Myo9b and
 RT identification of alternative splicing.";
 RL Gene 240:389-398(1999).
 CC -!- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
 CC MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS
 CC ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP
 CC AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.
 CC ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON RHO.
 CC -!- SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLOCALIZES WITH
 CC F-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS
 CC LOCALIZATION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE
 CC PERINUCLEAR REGION (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2/Q AND 3/C ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN, HEART, MUSCLE AND
 CC INNER EAR.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -!- SIMILARITY: CONTAINS 4 IQ DOMAINS.
 CC -----
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 CC -----
 CC EMBL; AF143687; AAF00122.1; -.
 CC EMBL; AF143685; AAF00120.1; -.
 CC EMBL; AF143686; AAF00121.1; ALT_FRAME.
 CC EMBL; AF143683; AAF00118.1; -.
 CC HSSP; P08799; LMND.
 CC MGD; MGI:106624; Myo9b.
 CC InterPro; IPR002219; DAG_PE_BIND.
 CC InterPro; IPR000048; IQ_region.
 CC InterPro; IPR000159; RA_domain.
 CC InterPro; IPR000198; RhGAP.
 CC InterPro; IPR001609; myosin_head.
 CC Pfam; PF00063; myosin_head; 2.
 CC Pfam; PF00130; DAG_PE_BIND; 1.
 CC Pfam; PF00612; IQ; 4.
 CC Pfam; PF00620; RhGAP; 1.
 CC Pfam; PF00788; RA; 1.
 CC PRINTS; PR00193; MYOSINHEAVY.

DR SMART; SM00242; MYSC; 1.
 DR SMART; SM00314; RA; 1.
 DR SMART; SM00324; RHOGAP; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PSS0081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PSS0096; IQ; 3.
 KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
 KW Cytoskeleton; Coiled coil; GTPase activation; Phorbol-ester binding;
 KW Zinc; Alternative splicing.
 FT DOMAIN 1 939
 FT DOMAIN 940 1044
 FT DOMAIN 1045 2158
 FT DOMAIN 1046 1071
 FT DOMAIN 1880 1901
 FT DOMAIN 1959 1989
 FT DOMAIN 844 855
 FT DOMAIN 957 977
 FT DOMAIN 979 1000
 FT DOMAIN 1001 1023
 FT DOMAIN 1024 1053
 FT DOMAIN 1633 1681
 FT DOMAIN 1713 1862
 FT NP_BIND 239 246
 FT VARSPPLIC 2022 2023
 FT VARSPPLIC 2024 2158
 FT CONFLICT 1937 1939
 FT CONFLICT 1947 1947
 FT CONFLICT 2040 2045
 FT CONFLICT 2049 2049
 FT CONFLICT 2067 2067
 FT CONFLICT 2157 2158
 SQ SEQUENCE 2158 AA; 243556 MW; 4978F1D770F56D28 CRC64;

Query Match 26.9%; Score 54; DB 1; Length 2158;
 Best Local Similarity 52.9%; Pred. No. 32;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 16 PCQLRCSNTPELTCOR 32
 |||||:||||:
 Db 1852 PCLLRCPDNDLTSMK 1868

Search completed: January 7, 2003, 09:38:05
 Job time : 4.55639 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 9.62907 Seconds

(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201

Sequence: 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72.5	36.1	499	11	O88714 mus musculus
2	64.5	32.1	5374	11	Q99ND0 mus musculus
3	61	30.3	966	5	Q22378 caenorhabdi
4	60	29.9	5146	6	Q8SPM4 bos taurus
5	59.5	29.6	353	5	Q9VW81 drosophila
6	59.5	29.6	353	5	Q8SZ58 drosophila
7	59	29.4	937	5	Q9GYR5 caenorhabdi
8	58	28.9	175	11	Q8R4W8 mus musculus
9	58	28.9	1299	5	Q26489 spodoptera
10	57.5	28.6	62	5	Q77419 ascaris suu
11	57.5	28.6	1376	5	Q8SZS2 drosophila
12	57.5	28.6	1679	5	Q24301 drosophila
13	57	28.4	321	10	Q9MAM0 arabidopsis
14	57	28.4	1717	5	Q26566 schistosoma
15	56	27.9	341	11	Q9D351 mus musculus
16	56	27.9	387	13	Q9PVD4 xenopus lae

17	55.5	27.6	146	12	Q9EP28
18	55.5	27.6	225	5	Q9VE40
19	55.5	27.6	955	4	Q96DN2
20	55.5	27.6	989	10	Q9ZU00
21	55.5	27.6	2820	5	Q9VLT6
22	55	27.4	330	5	O18118
23	55	27.4	344	11	Q924K7
24	55	27.4	450	4	Q8EUS3
25	55	27.4	1074	5	Q964D1
26	55	27.4	1101	5	Q964D2
27	55	27.4	1127	12	Q993K9
28	55	27.4	1513	5	O19770
29	54.5	27.1	146	12	Q9EP23
30	54.5	27.1	1752	4	Q9C091
31	54.5	27.1	1792	13	O57484
32	54.5	27.1	2155	4	O75443
33	54.5	27.1	2155	11	O08523
34	54	26.9	375	4	Q8WVD2
35	54	26.9	718	5	Q9B107
36	54	26.9	2447	5	Q9NEF9
37	54	26.9	4072	5	Q9W4Y4
38	53.5	26.6	146	12	Q9EP09
39	53.5	26.6	246	6	Q9TUX4
40	53.5	26.6	281	6	Q29475
41	53.5	26.6	285	6	Q95326
42	53.5	26.6	414	12	Q68813
43	53.5	26.6	1069	5	Q98PS2
44	53.5	26.6	2843	4	Q9Y6R7
45	53	26.4	305	2	Q9F917

ALIGNMENTS

RESULT 1

O88714
ID AC O88714 PRELIMINARY; PRT; 499 AA.
AD O88714
DT 01-NOV-1998 (TREMREL. 08, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DE Gastric mucin-like protein (fragment)
DE Gastric mucin-like protein (fragment)
GN GASTRIC MUCIN-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=STOMACH;
RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
RA Rio M.C.
RT "Identification of interactions between trefoil peptides and members
of the mucin protein family using the yeast two-hybrid system.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010752; CAA09343.1; -
DR HSSP; P56682; ICCV.
DR InterPro; IPR002919; TIL_Cysrich.
DR Pfam; PF01846; VWF_D.
DR Pfam; PF01846; TIL; 1.
DR Pfam; PF00094; vwd; 1.
DR SMART; SMO0216; VMD; 1.
FT NON_TER 1
FT NON_TER 499 499
SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 36.1%; Score 72.5; DB 11; Length 499;
Best Local Similarity 48.3%; Pred. NO. 0.0053;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;
Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLT 29
|||||
Db 430 CSQNEYFDHSEGTCTVPC-----APPTT 451

RESULT 2

099ND0 PRELIMINARY; PRT; 5374 AA.

ID 099ND0; PRELIMINARY; PRT; 5374 AA.

AC 099ND0; PRELIMINARY; PRT; 5374 AA.

DT 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE ZAN (Zonadhesin).

GN ZAN.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SV;

MDLINE=21138439; PubMed=11239002;

RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,

RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Teul L.-C.,

RA Miller W., Koop B.F.;

RT "Comparative analysis of the gene-dense ACHE/TPR2 region on human

RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";

RL Nucleic Acids Res. 29:1352-1365(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SV;

RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;

RT "Genomic Basis of Inter- and Intra-species Variation in Zonadhesin

RT Domain Structure.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.

DR EMBL; AF312033; AAK28824.1; -.

DR EMBL; AY046056; AAL04416.1; -.

DR MGD; MGI:106656; ZAN.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR003645; FOLN.

DR InterPro; IPR000998; MAM domain.

DR InterPro; IPR003328; TILA_Cyerich.

DR InterPro; IPR002919; TILA_Cyerich.

DR InterPro; IPR001007; VWF_C.

DR InterPro; IPR001846; VWF_D.

DR Pfam; PF00629; MAM_3.

DR Pfam; PF01826; TIL; 25.

DR Pfam; PF02345; TIL; 25.

DR Pfam; PF00094; wvd; 4.

DR SMART; SM00001; EGF-like; 1.

DR SMART; SM00274; FOLN; 21.

DR SMART; SM00137; MAM_3.

DR SMART; SM00214; VMC; 25.

DR SMART; SM00316; VMD_4.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; 18.

DR PROSITE; PS50060; MAM_2; 3.

DR EGF-like domain; Glycoprotein.

SO SEQUENCE 5374 AA; 579536 MW; 90D2D8CFE5DE24EB CRC64;

Query Match 32.1%; Score 64.5; DB 11; Length 5374;

Best Local Similarity 35.1%; Pred. No. 0.93;

Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 1 CSQNEVFDLHACIP-COLRCSNTP--PLTCQRYC 34

Db 3298 CPTNSQFTDCLPSCVPCSNCRCEVTSPSSCREGC 3334

RESULT 3

022378 PRELIMINARY; PRT; 966 AA.

ID 022378; PRELIMINARY; PRT; 966 AA.

AC 022378; PRELIMINARY; PRT; 966 AA.

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Hypothetical 102.5 kDa protein.

GN T10E10.4

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Telodermidae; Caenorhabditis.

OK NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RC MEDLINE=99069613; PubMed=9851916;

RA None;

RT "Genome sequence of the nematode C. elegans: a platform for

RT investigating biology. The C. elegans Sequencing Consortium.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Geisel C.;

RT "The sequence of C. elegans cosmid T10E10.";

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RT "Direct Submission.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; U39644; AAB80360.2; -.

DR HSRP; P10969; IMGT.

DR InterPro; IPR002557; Chitin_bind_Petr.

DR InterPro; IPR007574; ketoacyl-synt.

DR InterPro; IPR003571; Snake_toxin.

DR InterPro; IPR002899; WRI/EB.

DR Pfam; PF01607; GEM_14; 2.

DR SMART; SM00289; WRI; 12.

DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.

DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.

KW Hypothetical protein.

SO SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;

Query Match 30.3%; Score 61; DB 5; Length 966;

Best Local Similarity 37.5%; Pred. No. 0.63;

Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

QY 1 CSQNEVFDLHACIPCOLR--CSNTPPLTC 30

Db 216 CSQSTVENSDLVCPVLAIGNCDSSTQGPVC 247

RESULT 4

08SPM4 PRELIMINARY; PRT; 5146 AA.

ID 08SPM4; PRELIMINARY; PRT; 5146 AA.

AC 08SPM4; PRELIMINARY; PRT; 5146 AA.

DT 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE SCO-spndin.

GN SCO-SPONDIN.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;

OC Bovidae; Bovinae; Bos.

OK NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SUBCOMMISSURAL ORGAN;

RA Meinel A.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=SUBCOMMISSURAL ORGAN;

MDLINE=20465125; PubMed=11008217;

RA Gubron S.;


```
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Latreille P., Woldmann P., Zidanic M.;
RT "the sequence of C. elegans cosmid C23G10."
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT Direct Submission";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U99851; AAF99879.1; -.
KW Hypothetical protein.
SQ SEQUENCE 937 AA; 106668 MW; 1C140595DFD3ACE4 CRC64;

Query Match
Best Local Similarity 29.4%; Score 59; DB 5; Length 937;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 8 DSLHACIPCOLRCSNTPL 28
DB 439 ESVEHPLVPAIRCSADGPPL 459

RESULT 8
ID O8R4W8 PRELIMINARY; PRT; 175 AA.
AC O8R4W8;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE TRAF3 binding protein.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K., Irie S., Sato T.-A.;
RT "Identification of novel TRAF3 binding protein, T3BP, which increases
RT cellular F-actin content.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL83914.1; -.
SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EE93B1 CRC64;

Query Match
Best Local Similarity 28.9%; Score 58; DB 11; Length 175;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 CSQNEVFDLSLHACIPCOL 19
DB 22 CNOTCEPDLVRCVSCCL 40

RESULT 9
ID Q26489 PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Endoprotease furin.
GN FURIN.
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SF9;
RA Cieplik M., Klenk H.;
RT "Cloning and functional characterization of FURIN from Spodoptera
```

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RT frugiperda (SF9) cells.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68888; CAA93116.1; -.
DR HSSP; Q99405; IMPT.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR Pfam; PF01483; P_1_domain.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PRODOM; PD000717; P_domain; 1.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BEC572AB CRC64;

Query Match
Best Local Similarity 28.9%; Score 58; DB 5; Length 1299;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps 2;

OY 1 CSQNEVFDLSLHACIPCOLRCS-----SNTPPLTC 30
DB 1150 CSRPLRIDRLNNQCVCV---CSRGVTNSTPTPTDC 1181

RESULT 10
ID O77419 PRELIMINARY; PRT; 62 AA.
AC O77419;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Chymotrypsin/elastase inhibitor-1 (Fragment).
GN Asc/E-1.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98297373; PubMed=9635450;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RT "Antisarkis simplex: mutational bursts in the reactive site centers of
RT serine protease inhibitors from an ascarid nematode.";
RL Exp. Parasitol. 89:257-261 (1998).
DR EMBL; U94499; AAC61300.1; -.
DR HSSP; P07851; IEAI.
DR InterPro; IPR002919; TIL_Cystrich.
DR Pfam; PF01826; TIL; 1.
DR NON_TER 1
FT NON_TER 62
SQ SEQUENCE 62 AA; 6794 MW; 154CE25A375E0B2C CRC64;

Query Match
Best Local Similarity 28.6%; Score 57.5; DB 5; Length 62;
Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

OY 1 CSQNEVFDLSLHACIPCOLRCS--SNTP-PLTCR 32
DB 5 CGPNEVWTE---CTGCEMKCGDPENTPCPLMKRR 35

RESULT 11
ID O8S2S2 PRELIMINARY; PRT; 1376 AA.
AC O8S2S2;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE ID3018zp.
GN FUR2.
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RA Duan P., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altfelt H., Bel O., Chin C., Chou J., Choi E.,
 RA Com L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharaky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thavert A., Toriumi M., Vayberg M., Yu G., Federspiel N.A.,
 RA Theologis A., Becker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC T25K16 from chromosome
 RT 1";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC - SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
 DR EMBL: AC007323; AF26467.1; -.
 DR HSSP: P54274; IBA5.
 DR InterPro: IPR001005; Myb_DNA_binding.
 DR Pfam: PF00249; myb_DNA-binding; 1.
 DR SMART: SM00395; SANT; 1.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00090; MYB_3; 1.
 DR DNA-binding; Nuclear protein.
 KW SEQUENCE 321 AA; 36643 MW; F3411A75DBC0B406 CRC64;
 SQ
 Query Match 28.4%; Score 57; DB 10; Length 321;
 Best Local Similarity 41.4%; Pred. No. 0.92; Mismatches 6; Gaps 1;
 Matches 12; Conservative 1; Indels 10; Gaps 1;
 Oy 12 HACPICQLR-----GSSNPPLTCORYC 34
 Db 63 HACTVCDIADGVPCSGNCPPLAVHRKC 91
 RESULT 14
 ID Q26566 PRELIMINARY; PRT; 1717 AA.
 AC Q26566;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Epidermal growth factor receptor precursor.
 GN SER.
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.
 NC NCBI_TaxId=6183;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=PUERTO RICAN;
 RX MEDLINE=92365727; PubMed=1501637;
 RA Shoemaker C.B., Ramachandran H., Landa A., dos Reis M.G., Stein L.;
 RT "Alternative splicing of the Schistosoma mansoni gene encoding a
 RT homologue of epidermal growth factor receptor.";
 RT Mol. Biochem. Parasitol. 53:117-32(1992).
 RL EMBL: M86396; AA29866.1; -.
 DR HSSP: P11362; IFGK.
 DR InterPro: IPR000499; EGFR_L_domain.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002174; Furin-like.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam: PF00757; Furin-like; 2.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF01030; Recep_L_domain; 2.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00261; FU; 6.
 DR SMART: SM00219; TYKC; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE: PS00028; ZINC FINGER C2H2_1; UNKNOWN_1.
 KW ATP-binding; Receptor_Signal; Transferase; Tyrosine-protein kinase.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 1717 EPIDERMAL GROWTH FACTOR RECEPTOR.
 SQ SEQUENCE 1717 AA; 192304 MW; 1101A338C1653D8C CRC64;

Query Match 28.4%; Score 57; DB 5; Length 1717;
 Best Local Similarity 40.9%; Pred. No. 4.6;
 Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 Oy 1 CSQNEYPDSLHACPICQLRCSNTPPLTCORYC 22
 Db 646 CERNRYIDPQRHCLPCNCS 667
 RESULT 15
 ID Q9D351 PRELIMINARY; PRT; 341 AA.
 AC Q9D351;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 7420700M05RIK protein.
 GN 7420700M05RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euleleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=IN VITRO FERTILIZED EGGS;
 RX MEDLINE=C57BL/6J; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Katsukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuura Y., Nikaido I., Pleske G., Quackenbush J.,
 RA Schriml L.M., Staudt F.F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Baker K., Bollella D., Fujino M., Aono H., Bardelli R., Barch G.,
 RA Blake J., Bollella D., But C., Bojunga N., Carninci F., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK018361; BAB31177.1; -.
 DR HSSP: P08047; ISPL.
 DR MGD: MGI:1923003; 7420700M05RIK.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam: PF00096; Zf_C2H2_3.
 DR ProDom: PD000003; Znf_C2H2_1.
 DR SMART: SM00355; Znf_C2H2_3.
 DR PROSITE: PS00028; ZINC FINGER C2H2_1; 2.
 DR PROSITE: PS0157; ZINC FINGER C2H2_2; 3.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SQ SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFC CRC64;
 Query Match 27.9%; Score 56; DB 11; Length 341;
 Best Local Similarity 29.4%; Pred. No. 1.4; Mismatches 17; Indels 0; Gaps 0;
 Matches 10; Conservative 7; Indels 17; Gaps 0;
 Oy 1 CSQNEYPDSLHACPICQLRCSNTPPLTCORYC 34
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 Job time: 11.6291 secs

us-09-855-158-7.ra1

Tue Jan 7 10:36:58 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:14 ; Search time 4.17544 Seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-7
Perfect score: 201
Sequence: 1 CSQNEYFDSLHACIPQRCSSNTPLTCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 262574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.5	33.1	166	2	US-08-810-572A-6
2	66.5	33.1	166	4	US-09-290-333-6
3	66.5	33.1	293	2	US-08-810-572A-2
4	66.5	33.1	293	4	US-09-290-333-2
5	56	27.9	2476	2	US-08-276-967-2
6	53.5	26.6	381	4	US-09-257-580-2
7	53.5	26.6	5405	4	US-08-718-388-9
8	52	25.9	547	4	US-09-877-730-26
9	52	25.9	624	4	US-09-877-730-24
10	52	25.9	712	4	US-09-877-730-16
11	52	25.9	826	4	US-09-877-730-12
12	52	25.9	904	4	US-09-877-730-6
13	52	25.9	991	4	US-09-877-730-12
14	52	25.9	1069	4	US-09-877-730-2
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17	51.5	25.6	63	2	US-08-915-142-12
18	51.5	25.6	77	2	US-08-465-380-40
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25	51.5	25.6	77	2	US-08-461-965-4
26	51.5	25.6	77	2	US-08-461-965-40
27	51.5	25.6	77	2	US-08-326-110A-33

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29	51.5	25.6	77	2	US-08-634-641-40
30	51.5	25.6	77	3	US-09-249-471-4
31	51.5	25.6	77	3	US-09-249-471-40
32	51.5	25.6	77	3	US-09-249-472-4
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36	51.5	25.6	77	3	US-08-809-455-4
37	51.5	25.6	77	3	US-08-809-455-40
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44	51.5	25.6	81	2	US-08-486-397-7
45	51.5	25.6	81	2	US-08-486-399-7

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

APPLICANT: von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

SEQUENCE APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-FEB-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-810-572A-6
Query Match 33.1%; Score 66.5; DB 2; Length 166;
Best Local Similarity 32.4%; Pred. No. 0.48;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
QY 1 CSONEYFDSLHACIPQCLRGSSNTPPLTCQRYC 34
DB 34 CPEQYWDPLGTGCMSCCKTICNHQS-QRTCAFC 66

RESULT 2

US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.
von Bulow, Goetz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

FILING DATE: 12-Apr-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq, David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-290-333-6

Query Match 33.1%; Score 66.5; DB 4; Length 166;

Best Local Similarity 32.4%; Pred. No. 0.48; 14; Indels 1; Gaps 1;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPQCLRGSSNTPPLTCQRYC 34

DB 34 CPEQYWDPLGTGCMSCCKTICNHQS-QRTCAFC 66

RESULT 3

US-08-810-572A-2

Sequence 2, Application US/08810572A

Patent No. 5969102

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.
von Bulow, Goetz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-Feb-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 293 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-810-572A-2

Query Match 33.1%; Score 66.5; DB 2; Length 293;

Best Local Similarity 32.4%; Pred. No. 0.84; 14; Indels 1; Gaps 1;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPQCLRGSSNTPPLTCQRYC 34

DB 34 CPEQYWDPLGTGCMSCCKTICNHQS-QRTCAFC 66

RESULT 4

US-09-290-333-2

Sequence 2, Application US/09290333

Patent No. 6316222

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.
von Bulow, Goetz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290.333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq. David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match 33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 0.84;
Matches 11; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEFYDLSLHACIPQLRCSSNTPTLTQRYC 34
Db 34 CPSEQYDPLIGTCMSCKTICNQS-QRTCAFC 66

RESULT 5
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garbers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: US/SD.418/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-967-2
Query Match 27.9%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 1.2e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSQNEFYDLSLHACIP-CQ---LRCSSNTPTLTQRYC 34
Db 1851 CSAHSVYTSCVPSCLPSCDPEGQCTGAGAPSTCEGC 1888

RESULT 6
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257,580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
US-09-257-580-2
Query Match 26.6%; Score 53.5; DB 4; Length 381;
Best Local Similarity 48.3%; Pred. No. 38;
Matches 14; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

QY 4 NEYFDSLHACIPQLRCSSNTPTLTQRCR 32
Db 118 NKLFQQLAKTC-EVQLWVSSPPPTCVR 145

RESULT 7
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IGF FC REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/718,388
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:

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Tue Jan 7 10:36:58 2003

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Page 4

TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-388-9

Query Match 26.6%; Score 53.5; DB 4; Length 5405;
Best Local Similarity 34.3%; Pred. No. 4.9e+02;
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

QY 1 CSQNEYPDSLHACI-PCQLRGSSNTPPLTCORYC 34
DB 3934 CPQNSHYE---LCADTCISGCSALSAFLQCPDGC 3964

RESULT 8
US-09-877-730-26
Sequence 26, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 547
TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-26

Query Match 25.9%; Score 52; DB 4; Length 547;
Best Local Similarity 33.3%; Pred. No. 80;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 NEYFDSLHACI-PCQLRGSSNTPPLTCORY 33
DB 503 NSFIDAKVLSGICISRSISIPPCVCKMY 532

RESULT 9
US-09-877-730-24
Sequence 24, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 624
TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-24

Query Match 25.9%; Score 52; DB 4; Length 624;
Best Local Similarity 33.3%; Pred. No. 91;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 NEYFDSLHACI-PCQLRGSSNTPPLTCORY 33
DB 580 NSFIDAKVLSGICISRSISIPPCVCKMY 609

RESULT 10
US-09-877-730-22
Sequence 22, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 712
TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-22

Query Match 25.9%; Score 52; DB 4; Length 712;
Best Local Similarity 33.3%; Pred. No. 1e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 NEYFDSLHACI-PCQLRGSSNTPPLTCORY 33
DB 668 NSFIDAKVLSGICISRSISIPPCVCKMY 697

RESULT 11
US-09-877-730-16
Sequence 16, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 826

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Page 6

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-117-080-12

Query March 25.64; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.54; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
QY 10 LHAACIFQALRCSSNT-PLLTQRYC 34
DB 24 MIEACIGNGRCNENVGPPYCCSGPC 49

Search completed: January 7, 2003, 09:42:03
Job time: 5.17544 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:40:20 ; Search time 2.55639 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-7
Sequence: 201
1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	201	100.0	51	10	US-09-854-864-6
3	201	100.0	58	10	US-09-854-864-21
4	201	100.0	81	10	US-09-854-864-13
5	201	100.0	181	10	US-09-854-864-5
6	201	100.0	184	9	US-10-077-438-1
7	201	100.0	184	9	US-10-077-438-7
8	201	100.0	184	9	US-10-077-137-1
9	201	100.0	184	9	US-10-077-137-7
10	201	100.0	283	10	US-09-854-864-9
11	181	90.0	207	9	US-10-077-438-3
12	181	90.0	207	9	US-10-077-137-3
13	136	67.7	185	10	US-09-854-864-11
14	136	67.7	281	10	US-09-854-864-10
15	93.5	46.5	117	10	US-09-854-864-12
16	66.5	33.1	37	9	US-09-779-050A-45
17	66.5	33.1	59	10	US-09-854-864-20
18	66.5	33.1	67	10	US-09-854-864-16
19	66.5	33.1	166	10	US-09-854-864-15

20	66.5	33.1	231	9	US-09-779-050A-43	Sequence 43, Appl
21	66.5	33.1	233	9	US-09-779-050A-42	Sequence 42, Appl
22	66.5	33.1	233	9	US-10-084-971-2	Sequence 2, Appl
23	66.5	33.1	233	10	US-09-879-919-22	Sequence 22, Appl
24	66.5	33.1	233	10	US-09-854-864-14	Sequence 14, Appl
25	66.5	33.1	233	10	US-09-961-376-2	Sequence 2, Appl
26	66.5	33.1	397	10	US-09-854-864-18	Sequence 18, Appl
27	59.5	29.6	418	9	US-09-886-429-2	Sequence 2, Appl
28	59.5	29.6	735	10	US-09-898-570-10	Sequence 10, Appl
29	59.5	29.6	845	10	US-09-898-570-12	Sequence 12, Appl
30	59.5	29.6	974	10	US-09-898-570-14	Sequence 14, Appl
31	59.5	29.6	1009	10	US-09-898-570-16	Sequence 16, Appl
32	59	29.4	38	9	US-09-779-050A-46	Sequence 46, Appl
33	55	27.4	162	10	US-09-798-789-10	Sequence 10, Appl
34	53.5	26.6	5405	9	US-10-025-380-1116	Sequence 1116, Ap
35	53.5	26.6	5405	10	US-09-923-217-1116	Sequence 1116, Ap
36	53	26.4	108	9	US-09-950-933A-61	Sequence 61, Appl
37	53	26.4	131	10	US-09-790-264-61	Sequence 61, Appl
38	52	25.9	115	9	US-09-950-933A-65	Sequence 65, Appl
39	51.5	25.6	136	10	US-09-893-737-302	Sequence 302, App
40	51	25.4	78	9	US-09-749-637A-324	Sequence 324, App
41	51	25.4	117	9	US-09-950-933A-62	Sequence 62, Appl
42	51	25.4	119	9	US-09-950-933A-63	Sequence 63, Appl
43	50.5	25.1	131	9	US-09-950-933A-66	Sequence 66, Appl
44	50	24.9	133	10	US-09-800-909-3	Sequence 3, Appl
45	50	24.9	153	10	US-09-884-987-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 100.0%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 2
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 6
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 100.0%; Score 201; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 1,6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 34
DB 5 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 38

RESULT 3
US-09-854-864-21
Sequence 21, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 21
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 100.0%; Score 201; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 1,8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 34
DB 1 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 34

RESULT 4
US-09-854-864-13
Sequence 13, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 201; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 34
DB 1 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 34

RESULT 5
US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 100.0%; Score 201; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 5,1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 34
DB 5 CSONEYFDSLHACIPQQLRCSNTPPLTCQRYC 38

RESULT 6
US-10-077-438-1
Sequence 1, Application US/10077438
Patent No. US20020165156A1
GENERAL INFORMATION:
APPLICANT: Mackay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Teschopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immuno regulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT FILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536

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; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

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Query Match          100.0%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 34
DB 8 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 41

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RESULT 7
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

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Query Match          100.0%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 34
DB 8 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 41

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RESULT 8
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An

```

```

; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

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Query Match          100.0%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 34
DB 8 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 41

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RESULT 9
US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

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Query Match          100.0%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 34
DB 8 CSONEYFDSLHACIPQCLRCSSNTPTPLTCQRYC 41

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RESULT 10
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:

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Tue Jan 7 10:36:58 2003

us-09-855-158-7.rapb

Page 4

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; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9
Query Match          100.0%; Score 201; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 38
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RESULT 11
US-10-077-438-3
; Sequence 3, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoep, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3
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Query Match          90.0%; Score 181; DB 9; Length 207;
Best Local Similarity 63.0%; Pred. No. 1e-13;
Matches 34; Conservative 0; Mismatches 20; Indels 20; Gaps 1;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 46 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 99
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; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoep, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3
Query Match          90.0%; Score 181; DB 9; Length 207;
Best Local Similarity 63.0%; Pred. No. 1e-13;
Matches 34; Conservative 0; Mismatches 20; Indels 20; Gaps 1;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 46 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 99
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RESULT 13
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11
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Query Match          67.7%; Score 136; DB 10; Length 185;
Best Local Similarity 70.6%; Pred. No. 9,8e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
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RESULT 14
US-09-854-864-10
; Sequence 10, Application US/09854864
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; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match      67.7%; Score 136; DB 10; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLLHACIPCOLRCSNTPPLTCQRYC 34
DB 5 CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36

RESULT 15
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match      46.5%; Score 93.5; DB 10; Length 117;
Best Local Similarity 69.7%; Pred. No. 0.00037;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY 2 SONEYFDSLLHACIPCOLRCSNTPPLTCQRYC 34
DB 2 AQCEYFDSLLHAC-PC-LRCS---PPTCO-YC 27

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 09:38:19 ; Search time 4.43108 Seconds
(without alignments)
543.836 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201
Sequence: 1 CSONEYFDSLHACIPQLRCSSNTPLTCORVC 34

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Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New.*

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2: /cgn2_6/prodata/2/paa/US07 NEW COMB.pcp.*
3: /cgn2_6/prodata/2/paa/US08 NEW COMB.pcp.*
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6: /cgn2_6/prodata/2/paa/US11 NEW COMB.pcp.*
7: /cgn2_6/prodata/2/paa/US12 NEW COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	34	1	PCT-US02-34376-11
2	201	100.0	34	6	US-10-281-053-11
3	201	100.0	184	1	PCT-US02-34376-6
4	201	100.0	184	1	PCT-US02-06001-39
5	201	100.0	184	5	US-09-848-271-2
6	201	100.0	184	6	US-10-281-053-6
7	201	100.0	184	6	US-10-087-080-39
8	67.5	33.6	1548	6	US-10-180-903-2
9	66.5	33.1	33	1	PCT-US02-34376-13
10	66.5	33.1	33	6	US-10-281-053-13
11	66.5	33.1	166	6	US-10-293-816-6
12	66.5	33.1	293	6	US-10-268-951-22
13	66.5	33.1	293	6	US-10-258-368-1
14	66.5	33.1	293	6	US-10-293-816-2
15	66.5	33.1	301	6	US-10-258-368-12
16	66.5	33.1	334	6	US-10-258-368-8
17	66.5	33.1	366	6	US-10-258-368-6
18	66.5	33.1	404	6	US-10-258-368-15
19	59	25.4	34	1	PCT-US02-34376-14
20	59	25.4	34	6	US-10-281-053-14
21	55	27.4	162	6	US-10-258-102-420
22	53.5	26.6	4360	5	US-08-724-676-66993
23	53.5	26.6	4360	5	US-08-724-676-A-66993
24	53	26.4	131	6	US-10-269-353-61
25	52.5	26.1	976	6	US-10-276-774-1565
26	51	25.4	87	1	PCT-US02-32727-2251

27	51	25.4	87	6	US-10-057-498-2251	Sequence 2251, Ap
28	51	25.4	334	1	PCT-US02-32727-21573	Sequence 21573, A
29	51	25.4	334	6	US-10-057-498-21573	Sequence 21573, A
30	50.5	25.1	133	6	US-10-209-582-950	Sequence 950, App
31	50.5	25.1	710	1	PCT-US02-29560-308	Sequence 308, Appl
32	50	24.9	161	5	US-09-898-234B-4	Sequence 4, Appl
33	50	24.9	161	5	US-09-898-234B-4	Sequence 4, Appl
34	50	24.9	161	5	US-09-898-234B-4	Sequence 73, Appl
35	50	24.9	161	5	US-09-898-234B-4	Sequence 73, Appl
36	50	24.9	161	5	US-09-898-234B-4	Sequence 6, Appl
37	50	24.9	162	5	US-09-898-234B-6	Sequence 6, Appl
38	50	24.9	162	5	US-10-218-102-419	Sequence 419, App
39	50	24.9	162	6	US-10-218-102-424	Sequence 424, App
40	50	24.9	162	6	US-10-218-102-425	Sequence 425, App
41	50	24.9	162	6	US-10-218-102-427	Sequence 427, App
42	50	24.9	162	6	US-10-218-102-431	Sequence 431, App
43	50	24.9	162	6	US-10-218-102-432	Sequence 432, App
44	50	24.9	172	5	US-09-898-234B-20	Sequence 20, Appl
45	50	24.9	173	5	US-09-898-234B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
PCT-US02-34376-11
; Sequence 11, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86-PCT PCT/US02/34376
; CURRENT APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2002-10-24
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-11
Query Match 100.0%; Score 201; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPQLRCSSNTPLTCORVC 34
DB 1 CSONEYFDSLHACIPQLRCSSNTPLTCORVC 34
RESULT 2
US-10-281-053-11
; Sequence 11, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86

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; CURRENT APPLICATION NUMBER: US/10/281,053
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-11
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Query Match          100.0%; Score 201; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4,9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY
1 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 34
|||||
Db      8 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 34
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RESULT 3
PCT-US02-34376-6
; Sequence 6, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALI-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-6
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Query Match          100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY
1 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 34
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Db      8 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 41
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RESULT 4
PCT-US02-06001-39
; Sequence 39, Application PC/TUS0206001
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
```

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; TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; FILE REFERENCE: 018501-000840PC
; CURRENT APPLICATION NUMBER: PCT/US02/06001
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
PCT-US02-06001-39
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Query Match          100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY
1 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 34
|||||
Db      8 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 41
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RESULT 5
US-09-848-271-2
; Sequence 2, Application US/09848271
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven
; APPLICANT: Baker, Kevin
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR18 and Methods Based Thereon
; FILE REFERENCE: PF526
; CURRENT APPLICATION NUMBER: US/09/848,271
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/254,931
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/236,038
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/201,852
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-271-2
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Query Match          100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 34
|||||
Db      8 CSONEYFDSLHACIPCOLRCSNTPPLTCORYC 41
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RESULT 6
US-10-281-053-6
; Sequence 6, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
```

Tue Jan 7 10:36:59 2003

us-09-855-158-7.rapn

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; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US/10/281,053
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-6

Query Match      100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 7
US-10-087-080-39
; Sequence 39, Application US/10087080
; GENERAL INFORMATION:
; APPLICANT: Mack, David H
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-00840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match      100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 8
US-10-180-903-2
; Sequence 2, Application US/10180903

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; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-180-903-2

Query Match      33.6%; Score 67.5; DB 6; Length 1548;
Best Local Similarity 37.8%; Pred. No. 2.3;
Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 32
Db 1152 CAAVEYWDGSHRCQPCCHKKRCSCGSPSEDQCYTCPR 1188

RESULT 9
PCT-US02-34376-13
; Sequence 13, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-13

Query Match      33.1%; Score 66.5; DB 1; Length 33;
Best Local Similarity 32.4%; Pred. No. 0.26;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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Db 1 CPBQYWDPLLCGTCMSCKTICNHQS-QRTCAAF 33

RESULT 10
US-10-281-053-13
; Sequence 13, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang

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; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86
; CURRENT APPLICATION NUMBER: US/10/281,053
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO: 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-281-053-13

Query Match          33.1%; Score 66.5; DB 6; Length 33;
Best Local Similarity 32.4%; Pred. No. 0.26;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 1 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 33

RESULT 11
; US-10-293-816-6
; Sequence 6 Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von, Bulow, Goltz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-816-6

Query Match          33.1%; Score 66.5; DB 6; Length 166;
Best Local Similarity 32.4%; Pred. No. 0.73;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 34 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 66

RESULT 12
; US-10-268-951-22
; Sequence 22 Application US/10268951
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PR253P2
; CURRENT APPLICATION NUMBER: US/10/268,951
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; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 10/082,260
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-268-951-22

Query Match          33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 34 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 66

RESULT 13
; US-10-258-368-1
; Sequence 1 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Renner, Paul
; TITLE OF INVENTION: TacI As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO: 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-258-368-1

Query Match          33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 34 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 66

RESULT 14
; US-10-293-816-2
; Sequence 2 Application US/10293816
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Tue Jan 7 10:36:59 2003

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; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Biom, Biolog, Coz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-816-2
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Query Match 33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
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Db 34 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 66
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RESULT 15
US-10-258-368-12
; Sequence 12: Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Kennert, Paul
; TITLE OF INVENTION: Tac1 As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCI/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-258-368-12
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Query Match 33.1%; Score 66.5; DB 6; Length 301;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
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Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 42 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 74
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Job time : 4.43108 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: January 7, 2003, 09:31:39 ; Search time 29.0301 Seconds
(without alignments)
371.797 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEYFDSLHACIPCOLR.....SEYFDSLHACFPATCPYC 81

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	205	41.2	302	AAE00507	Human BCMA-Immunoglobulin G
2	205	41.2	302	AAE00507	Mouse IgG signal/h
3	201.5	40.5	283	AAE15488	Human BCMA-Immunoglobulin G
4	201	40.4	34	AAE15485	Human B-cell matur
5	201	40.4	51	AAE15485	Human B-cell matur
6	201	40.4	58	AAE15501	Human B-cell matur
7	201	40.4	181	AAE15484	Amino acid sequenc
8	201	40.4	184	AAE08843	A human BCMA prote
9	201	40.4	184	AAE94001	Human BCMA protein
10	201	40.4	184	AAE09241	Human BCMA protein

11	201	40.4	184	AAE00506	Human B cell matur
12	201	40.4	184	AAE00506	Human B cell matur
13	201	40.4	184	AAE00506	Human B cell matur
14	201	40.4	184	AAE00506	Human B cell matur
15	159.5	32.0	157	AAE07000	Human B cell matur
16	153	30.7	124	AAE15492	Human-murine BCMA
17	153	30.7	117	AAE15491	Human-murine B cell
18	139.5	28.0	281	AAE15489	Mouse BCMA-human i
19	136	27.3	185	AAE15484	Amino acid sequenc
20	136	27.3	185	AAE15484	Murine B cell matur
21	136	27.3	185	AAE15490	Mouse B cell matur
22	100.5	20.2	334	AAE15490	Protein of hTACI (
23	100.5	20.2	366	AAE15490	Protein of hTACI (
24	98	19.7	249	AAO14132	A murine ztnf4, a
25	96.5	19.4	249	AAE94006	Human protein SEO
26	95	19.1	256	AAE94006	Novel human diagno
27	95	19.1	351	ABG23698	Novel human diagno
28	93	18.7	166	AAE15494	Human lymphocyte s
29	93	18.7	166	AAE15494	Human TACI extrac
30	93	18.7	265	AAE09244	Human TACI splice
31	93	18.7	291	AAU10949	Human AGP-3 recept
32	93	18.7	293	AAU10949	Human lymphocyte s
33	93	18.7	293	AAU10949	Human neutrophilic
34	93	18.7	293	AAU10949	A transmembrane ac
35	93	18.7	293	AAU10949	Human TACI protein
36	93	18.7	293	AAU10949	Human tumour necro
37	93	18.7	293	AAU10949	Human TACI-IgG Fc
38	93	18.7	293	AAU10949	Human TACI recepto
39	93	18.7	293	AAU10949	Human transmembran
40	93	18.7	293	AAU10949	Tumour necrosis fa
41	93	18.7	293	AAU10949	Human transmembran
42	93	18.7	293	AAU10949	Human AGP-3 relate
43	93	18.7	293	AAU10949	Protein of N-termi
44	93	18.7	293	AAU10949	Human TACI-immunog
45	93	18.7	404	AAO14136	Protein of a compl

ALIGNMENTS

RESULT 1	AAE00507	AAE00507 standard; Protein; 302 AA.
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AC	AAE00507	
XX	31-JUL-2001	(first entry)
DT	Human BCMA-Immunoglobulin G Fc region fusion construct.	
DE	Human; A proliferation inducing ligand receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; murine; tumour necrosis factor; B cell maturation protein; BCMA; fusion protein; immunoglobulin G; IgG; Fc region.	
XX	Chimeric - Homo sapiens.	
OS	Chimeric - Mus sp.	
XX	Key	Location/Qualifiers
FT	Protein	1..22
FT	Protein	/label= Signal peptide
FT	Protein	/note= "Derived from murine Ig kappa sequence"
FT	Protein	23..302
FT	Region	label= Mature_human_BCMA_IgG_Fc_fusion_protein
FT	Region	23..75
FT	Region	/note= "Derived from human BCMA protein"
FT	Region	76..302
FT	Domain	/note= "Derived from human IgG Fc region"
FT	Domain	24..302

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FT      /label= Cysteine rich domain
XX      /note= "Derived from human BCMA"
XX      MO200124811-A1.
XX      PD
XX      12-APR-2001.
XX      PF
XX      05-OCT-2000; 2000WO-US27579.
XX      PR
XX      06-OCT-1999; 99US-0157933.
XX      PR
XX      11-FEB-2000; 2000US-0181807.
XX      PR
XX      30-JUN-2000; 2000US-0215688.
XX      PA
XX      (BIOJ ) BIOGEN INC.
XX      (APOT-) APOTEC R & D SA.
XX      PI
XX      Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P,
XX      WPI; 2001-266242/27.
XX      DR
XX      N-PSDB; AAD03847.
XX      PT
XX      Treating a mammal for a condition associated with undesired cell
XX      proliferation such as cancer or carcinoma, comprises administering a
XX      composition comprising A proliferation inducing ligand Receptor
XX      (APRIL-R) antagonist -
XX      Example 1; Fig 3B; 85pp; English.
XX
XX      The invention relates to a method of treating a mammal for a condition
XX      associated with undesired cell proliferation such as cancer or
XX      carcinoma. The method involves administering a composition comprising
XX      A proliferation inducing ligand Receptor (APRIL-R) also referred as
XX      B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX      interaction between APRIL and its cognate receptor(s). This method is
XX      useful for treating undesired cell proliferation such as cancer or
XX      carcinoma of human lung carcinoma, colon carcinoma, breast carcinoma,
XX      prostate carcinoma, and other carcinomas whose proliferation is modulated
XX      by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX      disease, systemic lupus erythematosus-SLE), hypertension, cardiovascular
XX      diseases, renal disorders, B-cell lympho-proliferative disorders,
XX      immunosuppressive diseases, organ transplantation, inflammation and
XX      human immunodeficiency virus (HIV), and for treating, suppressing or
XX      altering an immune response involving a signalling pathway between
XX      APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
XX      The present sequence is a fusion construct containing human APRIL-R
XX      also referred as BCMA or BCM protein, Fc region of human immunoglobulin
XX      G (IgG) and a signal sequence from murine Ig kappa cDNA.
XX
XX      Sequence 302 AA;
XX
XX      Query Match 41.2%; Score 205; DB 22; Length 302;
XX      Best Local Similarity 67.8%; Pred. No. 2.3e-10;
XX      Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;
XX
XX      Oy      1 CSQNEVPSDLHACIPQQLRCSSNTPPLTCORYC-CEYFDSL-----LHACPCLRCSP 53
XX      Db      31 CSQNEVPSDLHACIPQQLRCSSNTPPLTCORICNASVTVSGVDKHTCP--PCPAP 87
XX
XX      RESULT 2
XX      AAB60699
XX      ID      AAB60699 standard; Protein; 302 AA.
XX      AC
XX      AAB60699;
XX      DT
XX      22-MAY-2001 (first entry)
XX      DE
XX      Mouse IgG signal/human BAF-R/human IgG Fc fusion protein, BAF-R-Fc.
XX      KM
XX      Human BAF-R; BAF-R receptor; TNF family; immunoregulatory agent;
XX      KM
XX      immune-related disorder; B-cell growth inhibitor;
XX      KM
XX      B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX      KM
XX      autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

```

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XX      renal disorder; immunosuppressive disorder; HIV infection;
XX      organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX      autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX      B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX      lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
XX      OS
XX      Chimeric - Homo sapiens.
XX      OS
XX      Chimeric - Mus sp.
XX      PN
XX      MO200112812-A2.
XX      PD
XX      22-FEB-2001.
XX      PF
XX      16-AUG-2000; 2000WO-US22507.
XX      PR
XX      17-AUG-1999; 99US-0149378.
XX      PR
XX      11-FEB-2000; 2000US-0181884.
XX      PR
XX      18-FEB-2000; 2000US-0183536.
XX      PA
XX      (BIOJ ) BIOGEN INC.
XX      (APOT-) APOTEC R & D SA.
XX      PI
XX      McKay F, Browning J, Ambrose C, Tschopp J, Schneider P,
XX      Thompson J;
XX      WPI; 2001-202866/20.
XX      DR
XX      N-PSDB; AAF59999.
XX      PT
XX      Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX      lympho-proliferative disorder by administering BAF-R-receptor
XX      polypeptide, chimeric molecule comprising receptor or anti-BAF-R
XX      antibody homolog -
XX      Example 4; Fig 2; 59pp; English.
XX
XX      The invention relates to the use of a BAF-R receptor (BAF-R, also known
XX      as BCMA) protein, or a BAF-R fusion protein as an agent for the
XX      treatment of a variety of immune-related disorders. BAF-R is a member of
XX      the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX      agent, and also plays a role in the development of hypertension and
XX      related disorders. BAF-R, fusion proteins containing it, and BAF-R-
XX      specific antibodies can be used for inhibiting B-cell growth, dendritic
XX      cell-induced B-cell growth and maturation, and immunoglobulin production,
XX      and in the treatment of autoimmune disorders, B-cell lymphoproliferative
XX      disorders, hypertension and renal disorders. The BAF-R proteins may also
XX      be used in the treatment of immunosuppressive disorders and HIV
XX      infection, and in patients undergoing organ transplantation. The BAF-R
XX      proteins or BAF-R specific antibodies may be used for treating,
XX      suppressing or altering an immune response involving a signalling pathway
XX      between BAF-R and BAF-R, thereby inhibiting inflammation. Since BAF-R
XX      inhibits B-cell growth and maturation it is useful for treating diseases
XX      such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
XX      Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
XX      progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
XX      human BAF-R may be used in gene therapy to treat tumours, lymphomas,
XX      autoimmune disorders and inherited B-cell-associated disorders. The
XX      present sequence represents the BAF-R fusion protein BAF-R-Fc,
XX      comprising a mouse IgG-kappa signal sequence, residues 1-153
XX      of human BAF-R and a human IgG Fc sequence.
XX
XX      Sequence 302 AA;
XX
XX      Query Match 41.2%; Score 205; DB 22; Length 302;
XX      Best Local Similarity 67.8%; Pred. No. 2.3e-10;
XX      Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;
XX
XX      Oy      1 CSQNEVPSDLHACIPQQLRCSSNTPPLTCORYC-CEYFDSL-----LHACPCLRCSP 53
XX      Db      31 CSQNEVPSDLHACIPQQLRCSSNTPPLTCORICNASVTVSGVDKHTCP--PCPAP 87
XX
XX      RESULT 3
XX      AAE15488

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AAE15488 standard; Protein; 283 AA.
AAE15486;
12-MAR-2002 (first entry)
Human BCMA-immunoglobulin Fc region fusion protein.
Human; transmembrane activator and intracellular CAML interactor; TAC1;
cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatitis;
prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
rheumatoid arthritis; atherosclerosis; fusion protein.
Homo sapiens.
WO200187979-A2.
22-NOV-2001.
14-MAY-2001; 2001WO-US15567.
12-MAY-2000; 2000US-204039P.
27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
(AMGE-) AMGEN INC.
Theill LE, Yu G;
WPI; 2002-066686/09.
Inhibiting activity of B cell maturation protein and/or transmembrane
activator and intracellular cyclophilin ligand interactor, by
administering a binding partner for APRIL, a tumor necrosis factor
family ligand -
Disclosure; Fig 10B; 94pp; English.
The invention relates to a method for inhibiting TAC1 (transmembrane
activator and intracellular CAML interactor) and/or B cell maturation
protein (BCMA) activity in a mammal. The method comprises administering
a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
BCMA extracellular consensus sequence, but not the extracellular region
of TAC1 or BCMA. The method is useful for inhibiting B-cell or T-cell
and/or BCMA in a mammal which is useful for treating B-cell or T-cell
lymphoproliferative disorders, one or more solid tumours such as lung,
gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
antagonists are useful for treating inflammation and immune function
diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
disease), drug and insect sting allergy, inflammatory bowel disease
(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
is human BCMA protein-immunoglobulin Fc region fusion protein.
Sequence 283 AA;
Query Match 40.5%; Score 201.5; DB 23; Length 283;
Best Local Similarity 60.6%; Pred. No. 4, 4e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;
OY 1 CSQNEVFDLLHACIPCLRCSSNTPPLTCQRYC-CEYEDSL- LHCPC 47
Db 5 CSQNEVFDLLHACIPCLRCSSNTPPLTCQRYCNSVSKVGNAGGGGDKTHCP- 63
OY 48 LRCSPP 53

Db 64 -PCPAP 68
RESULT 4
AAE15486
AAE15486 standard; peptide; 34 AA.
AAE15486;
12-MAR-2002 (first entry)
Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
Human; transmembrane activator and intracellular CAML interactor; TAC1;
cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatitis;
prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
rheumatoid arthritis; atherosclerosis.
Homo sapiens.
WO200187979-A2.
22-NOV-2001.
14-MAY-2001; 2001WO-US15567.
12-MAY-2000; 2000US-204039P.
27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
(AMGE-) AMGEN INC.
Theill LE, Yu G;
WPI; 2002-066686/09.
Inhibiting activity of B cell maturation protein and/or transmembrane
activator and intracellular cyclophilin ligand interactor, by
administering a binding partner for APRIL, a tumor necrosis factor
family ligand -
Claim 1; Fig 10A; 94pp; English.
The invention relates to a method for inhibiting TAC1 (transmembrane
activator and intracellular CAML interactor) and/or B cell maturation
protein (BCMA) activity in a mammal. The method comprises administering
a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
BCMA extracellular consensus sequence, but not the extracellular region
of TAC1 or BCMA. The method is useful for inhibiting B-cell or T-cell
and/or BCMA in a mammal which is useful for treating B-cell or T-cell
lymphoproliferative disorders, one or more solid tumours such as lung,
gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
antagonists are useful for treating inflammation and immune function
diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
disease), drug and insect sting allergy, inflammatory bowel disease
(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
is human BCMA protein-immunoglobulin Fc region fusion protein.
Sequence 34 AA;
Query Match 40.4%; Score 201; DB 23; Length 34;
Best Local Similarity 100.0%; Pred. No. 7, 8e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 5
AAE15485 standard; peptide; 51 AA.
AAE15485;
12-MAR-2002 (first entry)

Human B-cell maturation (BCMA) protein extracellular domain.

Human: transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.

Homo sapiens.
WO200187979-A2.
22-NOV-2001.
14-MAY-2001; 2001WO-US15567.
12-MAY-2000; 2000US-204039P.
27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
(AMGE-) AMGEN INC.
The11 LE, Yu G;
WPI; 2002-066686/09.

Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand -

Claim 1; Fig 10A; 94pp; English.

The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein extracellular domain.

Sequence 51 AA;
Query Match 40.4%; Score 201; DB 23; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38

RESULT 6
AAE15501 standard; peptide; 58 AA.
AAE15501;
12-MAR-2002 (first entry)

Human B cell maturation protein cysteine rich extracellular region.

Human: transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.

Homo sapiens.
WO200187979-A2.
22-NOV-2001.
14-MAY-2001; 2001WO-US15567.
12-MAY-2000; 2000US-204039P.
27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
(AMGE-) AMGEN INC.
The11 LE, Yu G;
WPI; 2002-066686/09.

Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand -

Disclosure; Fig 13; 94pp; English.

The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumors such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region.

Sequence 58 AA;

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Query Match 40.4%; Score 201; DB 23; Length 58;
Best Local Similarity 100.0%; Pred. No. 3,3e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYFDSLLHACIPQQRCSNTPPLTCQRYC 34
DB 1 CSQNEYFDSLLHACIPQQRCSNTPPLTCQRYC 34
RESULT 7
AAE15484 standard; Protein; 181 AA.
XX AAE15484;
XX 12-MAR-2002 (first entry)
XX Human B-cell maturation (BCMA) protein.
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammatory; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; dermatitis; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.
XX Homo sapiens.
XX Key Location/Qualifiers
XX 538
XX Region /note= "Cysteine-rich consensus region; This is region
XX is specifically claimed as SEQ ID NO: 7 in claim 1 of
XX the specification"
XX 52..72
XX Domain /label= Transmembrane_domain
XX WO200187979-A2.
XX PD 22-NOV-2001.
XX PF 14-MAY-2001; 2001WO-US15567.
XX PR 12-MAY-2000; 2000US-204039P.
XX PR 27-JUN-2000; 2000US-214591P.
XX PR 14-MAY-2001; 2001US-0214591.
XX (AMGE-) AMGEN INC.
XX Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand
XX Disclosure; Fig 10A; 94pp; English.
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70) a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function

CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein.
XX Sequence 181 AA;
XX Query Match 40.4%; Score 201; DB 23; Length 181;
XX Best Local Similarity 100.0%; Pred. No. 3,3e-10;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYFDSLLHACIPQQRCSNTPPLTCQRYC 34
DB 5 CSQNEYFDSLLHACIPQQRCSNTPPLTCQRYC 38
RESULT 8
AAB08843
ID AAB08843 standard; peptide; 184 AA.
XX AAB08843;
XX 02-JAN-2001 (first entry)
XX Amino acid sequence of human.
XX BCMA; necrosis factor-KB activator; NF-kB; gene expression; cancer;
XX anti-cell death gene; apoptosis; viral infection; inflammatory response;
XX rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX Homo sapiens.
XX Key Location/Qualifiers
XX 57..77
XX Domain /note= "putative transmembrane domain"
XX WO2000050633-A1.
XX PD 31-AUG-2000.
XX PF 24-FEB-2000; 2000WO-US04925.
XX PR 24-FEB-1999; 99US-0121485.
XX PA (GEO) GEN HOSPITAL CORP.
XX Seed B, Ting A;
XX WPI; 2000-558405/51.
XX Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
XX gene and reporter gene, and determining alteration in reporter gene
XX expression
XX Claim 32; Fig 7A; 53pp; English.
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA
XX is a necrosis factor (NF)-KB activator. The method of the invention is
XX used to identify compounds which modulate BCMA activity (and thus NF-kB
XX activity). The specification describes a method of identifying a
XX polypeptide which increases gene expression from a promoter. The method
XX involves contacting a library of with a cell which expresses a
XX recombinant anti-cell death gene and a reporter gene operably linked to
XX the promoter, and then determining whether the expression of the
XX reporter gene is altered as a result of contact with library. The method
XX is useful for identifying polypeptides which increase or decrease gene
XX expression from a promoter. The BCMA polypeptide or nucleic acid are
XX useful for preparing a pharmaceutical composition for treating cancer,

CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF- κ B expression and thus for drug
 CC designing.

Sequence 184 AA;
 50
 Query Match 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
 Db 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 9
 ID AAY94001 standard; Protein; 184 AA.
 AC AAY94001;
 DT 20-OCT-2000 (first entry)
 DE A human BCMA protein, a B cell protein related to TACI.
 KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW zntf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple myeloma;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neurotoxicity;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 KW
 OS Homo sapiens.
 XX
 PN WO200040716-A2.
 XX
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000; 2000WO-US00396.
 XX
 PR 07-JAN-1999; 99US-0226533.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gross JA, Xu W, Madden K, Yee DP,
 DR WPI: 2000-452538/39.
 DR N-PSDB; AAA58559.
 XX
 FT Inhibiting zntf4 activity in a mammal, to treat autoimmune diseases,
 FT renal disease, graft versus host disease, and inflammation, comprises
 FT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
 XX
 XX Disclosure; Page 152; 175pp; English.

The present sequence represents a human BCMA protein, a B cell protein
 related to transmembrane activator and CAML-interactor (TACI) receptor.
 TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 domains of BR43x2 (an isoform of TACI) receptor or BCMA (a related B
 protein) receptor contain a cysteine rich domain, and are used for
 inhibiting zntf4 activity. zntf4 is a TNF ligand, and are used for
 for inhibiting BR43x2, TACI or BCMA receptor. They may also be used
 with activated or resting B lymphocytes, effecting engagement associated
 antibody production. The antibody production is associated with an
 autoimmune disease selected from systemic lupus erythematosus, myasthenia
 gravis, multiple sclerosis and rheumatoid arthritis. The zntf4 activity
 and BR43x2, TACI or BCMA receptor-ligand engagement is associated with

CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, or
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli.

Sequence 184 AA;
 50
 Query Match 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 34
 Db 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 10
 ID AAE09241 standard; Protein; 184 AA.
 AC AAE09241;
 DT 19-NOV-2001 (first entry)
 DE Human BCMA protein.
 KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KW TNFR; TACI; BCMA; therapy; cancer; leukemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW psoriasis.
 KW
 OS Homo sapiens.
 XX
 PN WO200160397-A1.
 XX
 PD 23-AUG-2001.
 XX
 PF 28-NOV-2000; 2000WO-US32378.
 XX
 PR 16-FEB-2000; 2000US-018938.
 XX
 PR 22-AUG-2000; 2000US-0226986.
 XX
 PA (GENTH) GENTTECH INC.
 XX
 PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marelsers SA, Piccoli RM,
 PI Van M,
 DR WPI: 2001-541628/60.
 DR N-PSDB; AAD15902.
 XX
 FT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 FT activity, for treating autoimmune disorders and cancer, comprises
 FT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 FT antagonists -
 XX
 XX Example 2; Fig 2; 160pp; English.

The invention relates to methods of using one or more agonists or
 antagonists to modulate the activity of the members of TNF (tumour
 necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 e.g. TACI or BCMA. The method is useful for treating pathological
 conditions or diseases associated with increased TALL-1 and APRIL
 expression or activity. TALL-1 and APRIL antagonists are used to
 block the interaction between APRIL and TALL-1 with TACI or BCMA.
 They are useful for treating a mammal suffering from cancer such
 as leukaemia, lymphoma, myeloma, cancers of lung, colon and
 autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 psoriasis and lupus erythematosus. The present sequence is human

[illegible]

CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAF-R
CC proteins or BAF-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents human BAF-R.

XX Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYPDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 13
AAV71979
ID AAV71979 standard; Protein; 184 AA.

XX AAV71979;

DT 28-MAR-2001 (first entry)

XX Human B cell maturation factor (BCMA) protein.

XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALI-1;
KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..62 /label= Extracellular_domain

XX WO200068378-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12266.

XX 06-MAY-1999; 99US-0132892.

XX 01-MAY-2000; 2000US-0201012.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI; 2001-016094/02.

XX N-PsDB; AAD02125.

XX Isolated TALI-1 protein is used to identify compounds that regulate B
XX lymphocyte proliferation, used to treat B lymphocyte associated
XX autoimmune disorders -

XX Claim 37; Page 104-105; 112pp; English.

XX The present invention relates to Tumour necrosis factor (TNF) and
XX Apol-related leucocyte expressed Ligand 1 (TALI-1) nucleic acid
CC

CC molecules, proteins (including homologues), and their antibodies. The
CC invention in particular relates to methods for regulating the
CC interaction between TALI-1 and TALI-1 receptors (BCMA referred as B cell
CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
CC mediated immune responses. TALI-1 protein is useful for identifying
CC compounds that regulate B lymphocyte proliferation. It is also useful for
CC treating B lymphocyte associated autoimmune disorders like rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC post-streptococcal glomerulonephritis or polyarteritis nodosa.
CC The TALI-1 protein and its corresponding nucleic acid sequence are also
CC useful in diagnostic assays.

XX Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYPDSLHACIPQCLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYPDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 14

ABB81487
ID ABB81487 standard; Protein; 184 AA.

XX ABB81487;

DT 02-SEP-2002 (first entry)

XX Human BCMA receptor related protein SEQ ID NO:7.

XX Human; Znf12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiaschematic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

XX WO200238766-A2.

XX 16-MAY-2002.

XX 05-NOV-2001; 2001WO-US47018.

XX 07-NOV-2000; 2000US-246449P.

XX 20-DEC-2000; 2000US-257131P.

XX 28-JUN-2001; 2001US-301715P.

XX 29-AUG-2001; 2001US-315565P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Henne RM, Grant FJ;
XX WPI; 2002-508212/54.
DR

Tue Jan 7 10:36:45 2003

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma
XX
XX
XX Disclosure; Page 135-136; 154pp; English.
XX
XX The present invention describes a human tumor necrosis factor receptor
CC designated ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, anti-inflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antischismatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy; (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC ankyloids, hypertension, large vessel disease, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is
CC given in the exemplification of the present invention.

XX Sequence 184 AA;
SQ
Query Match 40.4%; Score 201; DB 23; Length 184;
Best Local Similarity 100.0%; Pred No. 3 4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 34
DB 8 CSQNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 41

RESULT 15
AAB60700
ID AAB60700 standard; Protein; 157 AA.
XX
AC AAB60700;
XX
DT 22-MAY-2001 (first entry)
XX
DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
XX
KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCMA;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; anti-inflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
XX
OS Homo sapiens.
XX
XX WO200112812-A2.
XX
PD 22-FEB-2001.
XX
XX 16-AUG-2000; 2000WO-0522507.
XX
XX 17-AUG-1999; 99US-0149378.
XX
PR 11-FEB-2000; 2000US-0181684.
PR
PR 18-FEB-2000; 2000US-0183536.
XX

PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
PI Thompson J;
XX
XX WPI; 2001-202866/20.
DR N-PSDB; AAF60000.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFF-receptor
PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
PT antibody homolog -
XX
XX Example 1; Fig 3; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFF-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFF-R
CC proteins or BAFF-R specific antibodies may be used for treating
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFF-R and BAFF thereby inhibiting inflammation. Since BAFF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents a human BAFF-R protein sequence as encoded
CC by plasmid pJST535. However, this BAFF-R protein sequence is 27 amino
CC acids shorter than that given in AAB60698.

XX Sequence 157 AA;
SQ
Query Match 32.0%; Score 159.5; DB 22; Length 157;
Best Local Similarity 90.6%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 QNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 34
DB 7 QNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 35

Search completed: January 7, 2003, 09:37:26
Job time : 29.0301 secs

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Tue Jan 7 10:36:47 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: January 7, 2003, 09:35:04 ; Search time 11.5714 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEVFDLLHACIPCOLR.....SEVFDLLHACPPATCQPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	201	40.4	184	2 S43486	B-cell maturation factor - human
2	94.5	19.0	223	2 B38346	ultra-high-sulfur keratin
3	94.5	19.0	230	2 A38346	ultra-high-sulfur keratin
4	92.5	18.6	169	1 S18946	ultra-high-sulfur keratin
5	91.5	18.4	186	2 A45910	ultra-high-sulfur keratin
6	89	17.9	1574	2 T13954	MEGF6 protein - rat
7	87	17.5	1680	2 A43434	furin (EC 3.4.21.7)
8	86.5	17.4	1548	2 S34583	serine proteinase
9	86	17.3	188	2 J65547	high sulfur protease
10	83	16.7	131	1 KRSH43	keratin high-sulfur
11	83	16.7	175	2 S37649	high-sulfur keratin
12	82	16.5	126	2 I46489	cysteine-rich hair
13	82	16.5	526	2 JC6133	deubiquitinating e
14	81	16.3	2823	2 T23064	hypothetical prote
15	81	16.3	2823	2 F87908	protein T22A3.8 [i
16	81	16.3	3102	2 T43291	laminin alpha chain
17	80.5	16.2	151	2 S60314	hair keratin cyste
18	80.5	16.2	937	2 I53282	gene PACB4 protein
19	80.5	16.2	1101	2 T16840	hypothetical prote
20	80.5	16.2	1798	2 S53869	laminin beta-2 cha
21	80	16.1	3075	2 S14458	laminin alpha-1 ch
22	79.5	16.0	965	2 S62935	hypothetical prote
23	79.5	16.0	1077	2 T41146	probable cysteine-
24	79.5	16.0	1077	2 T41146	hemocytin - silkw
25	79.5	16.0	3133	2 S52093	Notch homolog Motc
26	78.5	15.9	861	2 A48925	hypothetical prote
27	78.5	15.8	201	2 D71190	hypothetical prote
28	78.5	15.8	294	2 T23682	hypothetical prote
29	78	15.7	572	2 T29880	hypothetical prote
	78	15.7	1188	2 D86236	protein P14N23.5 [

30	77.5	15.6	132	1 KRGT3J	keratin high-sulfu
31	77.5	15.6	177	2 S37650	high-sulfur kerati
32	77	15.5	162	2 I47107	keratin high-sulfu
33	77	15.5	172	1 KRSHHA	zonadhesin - mouse
34	77	15.5	5376	2 T42215	PACB4A - mouse (fr
35	76.5	15.4	1513	2 I52527	hypothetical prote
36	76.5	15.4	1513	2 T23681	transcription adap
37	76.5	15.4	2474	2 A54277	high-sulfur wool m
38	76	15.3	172	2 I47106	high-sulfur wool m
39	76	15.3	182	2 I47105	furin (EC 3.4.21.7
40	76	15.3	1299	2 T43251	transcription coac
41	76	15.3	2440	2 S39162	CREB-binding prote
42	76	15.3	2441	2 S39161	otogelin - mouse
43	76	15.3	2910	2 T42214	hypothetical prote
44	75.5	15.2	654	2 T30136	adhesive ligand ep
45	75.5	15.2	1713	2 A55347	

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: S43486; S31208; S36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirec
A;Reference number: S43486; MUID:94218235; PMID:8165126
A;Accession: S43486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <LA3>
A;Cross-references: EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:9471245
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
EMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:g29408
A;Accession: S36661
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 4-184 <LA3>
A;Cross-references: EMBL:Z14955
C;Genetics:
A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor

Query Match 40.4%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.1e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 2
B38346
ultra-high-sulfur keratin 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38660; B38346
R;Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogeli, G.

us-09-855-158-13.rpr

Tue Jan 7 10:36:47 2003

```
RESULT 6
MEG6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genome 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:93449293; PIDN:BAA32462.1; PID:93449294
A:Experimental source: strain Spregue-Dawley; brain
C:Genetics:
A:Gene: MEG6

Query Match 17.9%; Score 89; DB 2; Length 1574;
Best Local Similarity 29.4%; Pred. No. 1.8; Indels 38; Gaps 8;
Matches 30; Conservative 9; Mismatches 30; FDSLLHACPC 47

QY 1 CSQNEYFDSLLHACIPCOL-----RCSNTPLT---CQRYCCEY----FDSLLHACPC 47
Db 966 CSAGAPCDVATGSCI-CPAGRWPCRAQSCPLTFLGLNCSQICTCFNGASCDSVTGQC-- 1022
QY 48 LRCSP-----PTCQYCCFHSEYFDSLLHACPPA-----TCQPYC 81
Db 1023 -HCAPGWMGPTC-----LQACPGLYGKNQCHSC 1050

RESULT 7
A43434
furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Roebroek, A.J.; Greemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:Cross-references: GB:M94375; NID:9157461; PID:9157462
A:Note: Sequence extracted from NCBI backbone (NCBIN:111933, NCBIPI:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Superfamily: FlyBase:Fgn0004598
A:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
P:409-652/Domain: subtilisin homology <Sm>
P:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 17.5%; Score 87; DB 2; Length 1680;
Best Local Similarity 25.0%; Pred. No. 2.9; Indels 50; Gaps 9;
Matches 31; Conservative 12; Mismatches 12; -ACP--- 46

QY 1 CSQNEYFDSLLHACIPCOLRCSNTPLTTCQ---RYC--CEYFDSLLH-----ACP--- 46
Db 1051 CPDGYFENSRRNRTCVPCENFNCAS-----CQDHPEYTCSDH-HLVNHEHKYCSACFLDT 1103
QY 47 -----CLRCSPTTCQVC--CFHSEYF--DLSLLHACPPA-----TC 77
Db 1104 YETEDNKAFCFHCSTCATCNGFTDQDITCRSSRYAWQNKCLISCPDGFYADKKRLECMPC 1163
QY 78 QPYC 81
Db 1164 QEGC 1167

RESULT 8
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a t
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:D17583; NID:9407344; PIDN:BAA04507.1; PID:d1005033; PID:9440374
A:Keywords: hydrolase; serine proteinase
C:Keywords: hydrolase; serine proteinase

Query Match 17.4%; Score 85.5; DB 2; Length 1548;
Best Local Similarity 22.1%; Pred. No. 3; Indels 53; Gaps 3;
Matches 29; Conservative 6; Mismatches 42

QY 1 CSQNEYFDSLLHACIPCOLRCSNTPLTLCQRYCCEYFDSLL----- 42
Db 1152 CAAYVWDEGSHRCOPCHKKCRSCGSEDDCYTCPRFTFLNTTCVKECPGYHTDKDS 1211
QY 43 -----HACPLRCSP-----PTCQYCCFHSEYFDSLLHACPC----- 73
Db 1212 QQCVLCHSSCRTEGPHSMQCLSCRPGWFLQKKECLLQCRDGYGEGTSGRCEKCDKSK 1271
QY 74 -----PATCQ 78
Db 1272 SCRGRPTDCQ 1282

RESULT 9
JC6547
high sulfur protein B2E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JC6547
R:Mitsui, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tauboi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A:Title: Structure and hair follicle-specific expression of genes encoding the rat high s
A:Reference number: JC6547; MUID:98201805; PMID:9524245
A:Accession: JC6547
A:Molecule type: DNA
A:Residues: 1-188 <MIT>
A:Cross-references: DBJ:AB003753; NID:93046870; PIDN:BAA25573.1; PID:93046871
A:Comment: This protein is a cysteine-rich, keratin associated protein.
C:Genetics:
A:Gene: b2E
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: hair

Query Match 17.3%; Score 86; DB 2; Length 188;
Best Local Similarity 22.5%; Pred. No. 0.73; Indels 62; Gaps 7;
Matches 29; Conservative 10; Mismatches 28; ---R 32

QY 1 CSQNEYFDSLLHACIP-----COLRCSNTPLTTCQ----- 32
Db 69 CSQSS-----CCQPSCCCTSCCQPTCCQNS---SCQSCCGTSGGEGSGATSCRV 118
QY 33 YC---CEYFDSLLHACPLCRCSPTC-----QYCCFHSEYFDSLLHAC 72
Db 119 WCRPDVRVETCLPPCCVWCTPTTCCOLHQAQSCCRPSYCGQSCCRPA---CCCHCC 174
QY 73 PATCQPYC 81
Db 175 EPSCRFSC 183
```

```

RESULT 10
KRSFA3
Keratin high-sulfur matrix protein IIA3 - sheep
N/Alternate names: M2.6 protein
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996
C/Accession: A02840
R/Swartz, J.S.; Haylett, T.
Biochem. J. 133, 641-654, 1973
A/Title: Studies on the high-sulfur proteins of reduced merino wool. Amino acid sequenc
A/Reference number: A90269; MUID:74022242; PMID:4584026
A/Accession: A02840
A/Molecule type: protein
A/Residues: 131 <SWA>
A/Experimental: 131
C/Comment: Wool source: Merino wool
C/Superfamily: keratin high-sulfur matrix protein IIA
C/Keywords: duplication, hair

Query Match
Best Local Similarity 16.7%; Score 83; DB 1; Length 131;
Matches 26; Conservative 12; Mismatches 35; Indels 30; Gaps 6;

OY 1 CSQNEYPDSLHACIPQQR---CSSNTPPLT-----COR-YCCSEYFSLHMA 44
DB 18 CLOPRYRD-----PCCRPVSCOTVRPVTFRCTRPICPCRRPVCCDPCSLQEGC 71
OY 45 CCLCRSPPTQY-----CCPHSEYFSLHACP---PATCOP 79
DB 72 CRPTCCPTSCQAVVCRRCMAITCCQPVSVCCPCRCRPTSCQF 114

RESULT 11
S37649
high-sulfur keratin - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C/Accession: S37649
R/Zhambadava, B.D.; Genlin, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A/Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A/Reference number: S37649
A/Accession: S37649
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 175 <ZHU>
A/Cross-references: EMBL:X63338; NID:G311881; PIDD:CAA44938.1; PID:G311882
C/Superfamily: keratin high-sulfur matrix protein IIA

Query Match
Best Local Similarity 16.7%; Score 83; DB 2; Length 175;
Matches 22; Conservative 6; Mismatches 24; Indels 16; Gaps 5;

OY 17 COLGSSNTPPLTCORYCCSEYFSLHACPCRLRCSPPTQ--YCCF-HSEYFSLHACP 73
DB 25 CQPCCTCT---CQPCSCB-----TSC---CQPCCTCTCFQFLASQVLDQLSCCQ 71
OY 74 PATCOPYC 81
DB 72 PSCCETSC 79

RESULT 12
146489
cysteine-rich hair keratin associated protein - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 24-Sep-1999
C/Accession: I46489; S49201
R/Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A/Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A/Reference number: I46489; MUID:95228955; PMID:7536172
A/Accession: I46489

```

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A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-126 <POK>
A/Cross-references: EMBL:X80035; NID:G510540; PIDD:CAA56339.1; PID:G510541
C/Superfamily: ultra-high-sulfur keratin

Query Match
Best Local Similarity 16.5%; Score 82; DB 2; Length 126;
Matches 23; Conservative 6; Mismatches 23; Indels 24; Gaps 6;

OY 14 CIP--COLGSSNTPPLTCORYCCSEYFSLHACPCRLRCSPPTQ-----YCCPHSEYF 65
DB 26 CRPCRCRPPCCQ---PSCRPIC-----ISSC---CRPCCQSVCCPCRCRPSCYI 72
OY 66 DSLHACPPATCOPYC 81
DB 73 SS---CCRPICRPTC 85

RESULT 13
JC6133
deubiquitinating enzyme - mouse
N/Alternate names: DOB-1 protein
C/Species: Mus musculus (house mouse)
C/Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
C/Accession: JC6133
R/Zhu, Y.; Cantrell, M.; Papa, F.R.; Hochstrasser, M.; D'Andrea, A.D.
Proc. Natl. Acad. Sci. U.S.A. 93, 3275-3279, 1996
A/Title: DOB-1, a deubiquitinating enzyme with growth-suppressing activity.
A/Reference number: JC6133; MUID:96194957; PMID:8622927
A/Accession: JC6133
A/Molecule type: mRNA
A/Residues: 1-526 <ZHU>
A/Cross-references: GB:U41636; NID:G1302629; PIDD:ACG52532.1; PID:G1302630
C/Comment: This enzyme is the first enzyme of the ubiquitin system directly implicated
C/Genetic: dub-1
A/Genes: dub-1

Query Match
Best Local Similarity 16.5%; Score 82; DB 2; Length 526;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

OY 19 LKCSNTPPLTCORYCCSEYFSLHACPCRLRCSPPTQYCCPHSEYFSLHMA 71
DB 66 LQCLTHPPL-----ADVVLQSHSQC--CSPECCKLCAMEALVTQSLHS 110

RESULT 14
T23064
hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C/Accession: T23064; T25096
R/Barron, K.
Submitted to the EMBL Data Library, October 1997
A/Reference number: T23064
A/Accession: T23064
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 2823 <MTL>
A/Cross-references: EMBL:AL008585; PIDD:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8
R/McMurry, A.
Submitted to the EMBL Data Library, October 1996
A/Reference number: T25096
A/Accession: T25096
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2823 <MTL>
A/Cross-references: EMBL:Z81125; PIDD:CA803385.1; GSPDB:GN00019; CESP:T22A3.8

```

US-09-855-158-13.fpr

Tue Jan 7 10:36:47 2003

A:Experimental source: clone T22A3
C:Genetics:
A:Gene: CESP:T22A3.8
A:Map position: 1 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
A:Introns: 45/1; 282/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;
Best Local Similarity 27.7%; Pred. No. 14;
Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;
QY 1 CSQNEYFDSLHACIPCOLRCSNTPL---TCQRYCCEYFDSLHACPLRC-----SPP 53
Db 873 CSDGFFEDPLTGKIEC--TCNGNIDPMGIGNC-----DS--ETGKCLKICHTIGD 920
QY 54 TCQYCCFHSEYFDSLHACPPATC-----QPYC 81
Db 921 SCESCKEH-HWGNALHTCKPCGCHTQGA VNPQC 953

RESULT 15
protein T22A3.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
C:Accession: F87908
C:Accession: The C. elegans Sequencing Consortium.
C:Accession: 2012-2018, 1998
C:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F87908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <STO>
A:Cross-references: GB:chr_1; PIDN:CAA15432.1; PID:G3924779; GSPDB:GN00019; CESP:T22A3.8
A:Accession: E87908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <ST2>
A:Cross-references: GB:chr_1; PIDN:CAB03385.1; PID:G3924881; GSPDB:GN00019; CESP:T22A3.8
C:Genetics:
A:Gene: T22A3.8
A:Map position: 1
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;
Best Local Similarity 27.7%; Pred. No. 14;
Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;
QY 1 CSQNEYFDSLHACIPCOLRCSNTPL---TCQRYCCEYFDSLHACPLRC-----SPP 53
Db 873 CSDGFFEDPLTGKIEC--TCNGNIDPMGIGNC-----DS--ETGKCLKICHTIGD 920
QY 54 TCQYCCFHSEYFDSLHACPPATC-----QPYC 81
Db 921 SCESCKEH-HWGNALHTCKPCGCHTQGA VNPQC 953

Search completed: January 7, 2003, 09:41:10
Job time : 13.5714 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 6.09023 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEYFDLLHACIPQCLR.....SEYFDSLLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	40.4	184	1	Q02223 homo sapien
2	136	27.3	185	1	Q88472 mus musculus
3	98	19.7	249	1	Q02335 mus musculus
4	93	18.7	293	1	Q14336 mus musculus
5	92.5	18.6	169	1	P26371 homo sapien
6	91	18.3	194	1	P75690 homo sapien
7	87	17.5	1680	1	P30432 drosophila
8	86.5	17.4	1877	1	Q04592 mus musculus
9	83	16.7	131	1	P02441 ovine arties
10	82	16.5	526	1	Q61068 mus musculus
11	81	16.3	1587	1	Q09666 mus musculus
12	80.5	16.2	937	1	Q63415 rattus norv
13	80.5	16.2	1798	1	P55268 mus musculus
14	80	16.0	3075	1	P25391 homo sapien
15	79.5	16.0	965	1	P53971 saccharomy
16	79.5	16.0	3133	1	P98092 bombyx mori
17	79	15.9	1696	1	Q94315 branchiosto
18	77.5	15.6	132	1	P02442 capra hircu
19	77.5	15.6	139	1	O43609 homo sapien
20	77	15.3	171	1	P02438 ovine arties
21	77	15.3	5376	1	O88799 mus musculus
22	76.5	15.4	2411	1	P45481 mus musculus
23	76	15.3	2441	1	Q16787 homo sapien
24	75.5	15.2	1713	1	Q9r0b6 mus musculus
25	75	15.1	1581	1	P11047 homo sapien
26	75	15.1	1609	1	Q28055 mus musculus
27	74.5	15.0	610	1	P07942 homo sapien
28	74	14.9	1786	1	Q92793 homo sapien
29	74	14.9	2442	1	Q9qxy9 mus musculus
30	73.5	14.8	313	1	Q61292 mus musculus
31	73.5	14.8	1799	1	P29122 homo sapien
32	72.5	14.6	969	1	Q98930 g sortilin-
33	72.5	14.6	1592	1	

34	72	14.5	575	1	TRBM_HUMAN
35	72	14.5	867	1	SSPO_BOVIN
36	72	14.5	1367	1	IG1R_HUMAN
37	72	14.5	1700	1	BAR3_CHITE
38	72	14.5	2569	1	LMA3_MOUSE
39	72	14.5	4655	1	LSP2_HUMAN
40	71.5	14.4	1435	1	BBAL_PLAFC
41	71	14.3	62	1	IBB_MEDSC
42	71	14.3	63	1	ICE1_ASCSU
43	71	14.3	810	1	NEL1_HUMAN
44	71	14.3	3712	1	LNA_DROME
45	70.5	14.2	96	1	IBBA_PEA

ALIGNMENTS

RESULT 1
ID TRI7_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation, is bidirectionally transcribed.);
DE TNFRSF17 OR BCMA OR BCM.
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX 11;
RN SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RSSE=Peripheral blood leukocytes, and Lymph node;
RC MEDLINE=93010984; PubMed=1396583;
RA Laabi Y, Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
FT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma";
RL EMO J. 11:3897-3904(1992).
RN SEQUENCE FROM N.A.
RP MEDLINE=94218235; PubMed=8165126;
RX Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RA "The BCMA gene preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";
RT Nucleic Acids Res. 22:1147-1154(1994).
RL [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=9425270; PubMed=10493829;
RX Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.S., Harris P.C., Venter J.C., Adams M.D.;
RA "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q";
RT Genomics 60:295-308(1999).
RL [4]
RN SEQUENCE FROM N.A., AND VARIANT THR-153.
RP MEDLINE=21419161; PubMed=11528522;
RX Kawasaki A., Tsuchiya N., Fukazawa K., Hashimoto H., Tokunaga K.;
RA "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis";
RT Genes Immun. 2:276-279(2001).
RL [5]
RN FUNCTION.
RP MEDLINE=20363816; PubMed=10903733;
RX Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C., Inoue J., Devereux O., Tsapis A.;
RA "TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION
 RX MEDLINE=20259066; PubMed=10901128;
 RA Gross J.A., Johnston J., Madri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lotton-DeF C.,
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kundavogel W., Clegg C.H.;
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Saxosi I., Heu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF6 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.;
 RT "B-cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL: Z14954; CAI78679.1; -
 DR EMBL: Z28575; CAI82691.1; -
 DR EMBL: Z28574; CAI82690.1; -
 DR EMBL: U05742; AAB67251.1; -
 DR EMBL: AB052772; BAB60895.1; -
 DR PIR: S31208; S31208.
 DR PIR: S31209; S31209.
 DR Genew; HGNC:11913; TNFRSF17.
 DR MM; 109545; -
 KM Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KM Transmembrane; Chromosomal translocation; Polymorphism;
 FT DOMAIN 1 54
 FT TRANSMEM 55 77
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 78 184
 FT REPEAT 79 41
 FT SITE 3 4
 FT INTERPEPTIN 2/BCM ONCOGENE.
 FT DISULFID 8 21
 FT DISULFID 24 37
 FT DISULFID 28 41
 FT VARIANT 153 153
 FT A->T.
 FT /FTID=VAR_012234.
 SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 40.4%; Score 201; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.2e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSNFFPSLHACTPOLRCSSNTPPLTCORC 34
 DB 8 CSNFFPSLHACTPOLRCSSNTPPLTCORC 41
 RESULT 2
 TR17 MOUSE STANDARD; PRT; 185 AA.
 ID TR17 MOUSE
 AC O88472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 OS TNFSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BAIB/C; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabli Y., Callebaut I., Roussel J., Hatzoglu A.,
 RA Le Contat M., Morron J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukuishi Y., Kono H., Adachi Y., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batálov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gileadi C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Strubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Baisn G.,
 RA Blake J., Botfield D., Bouungu N., Caminati P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons F., Marchionni L., Mashima U., Mazzarelli U., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlschki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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EMBL; AF061505; AAC23799.1; -
EMBL; AK020247; BAB32038.1; -
MGD; MGI:1343050; Tnf1rfl7.
KW Receptor; Immune response; Signal-anchor; Transmembrane;
Alternative splicing.
FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 71 185 CYTOPLASMIC (POTENTIAL).
FT REPEAT 4 36 TNFR-CYS.
FT DISULFID 5 18 BY SIMILARITY.
FT DISULFID 21 32 BY SIMILARITY.
FT DISULFID 25 36 BY SIMILARITY.
FT VARSPLIC 87 91 MISSING (IN ISOFORM 2).
SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 27.3%; Score 136; DB 1; Length 185;
Best Local Similarity 70.6%; Pred. No. 8.1e-07;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
QY 1 CSONEYFDSLLHACIPCOLRCSSNTPLTCQRYC 34
DB 5 CPHSEYFDSLLHACKPCHLACSN--PPATCPQYVC 36

RESULT 3

ID T13X_MOUSE STANDARD; PRT; 249 AA.
AC Q9ET33; Q9DB23;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
activator and CAML interacto).
GN TNFRSF13B OR TACI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=21177254; PubMed=10881172;
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
Dixit V.M.;
RT "Identification of a receptor for Blys demonstrates a crucial role in
humoral immunity";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radocica K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schiraldi L., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,

RA Hayaishizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RP FUNCTION
RX MEDLINE=20341628; PubMed=10880535;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
Meng S.-Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21322748; PubMed=11429548;
RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT "TACI-ligand interactions are required for T cell activation and
collagen-induced arthritis in mice.";
RL Nat. Immunol. 2:632-637(2001).
CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
that binds both ligands with similar high affinity. Mediates
calcineurin-dependent activation of NF-AT, as well as activation
of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
cell function and the regulation of humoral immunity (by
similarity).
CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
domain of CAMLG with its C-terminus (By similarity).
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

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EMBL; AF257673; AK000081.1;
EMBL; AK004668; BAB23457.1;
MGD; MGI:1889411; Tnf1rfl3b
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
FT DOMAIN 1 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 150 249 CYTOPLASMIC (POTENTIAL).
FT REPEAT 5 38 TNFR-CYS 1.
FT REPEAT 42 76 TNFR-CYS 2.
FT DISULFID 6 19 BY SIMILARITY.
FT DISULFID 22 34 BY SIMILARITY.
FT DISULFID 26 38 BY SIMILARITY.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 65 76 BY SIMILARITY.
FT CONFLICT 137 137 I -> F (IN REF. 2).
SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931DB1 CRC64;

Query Match 19.7%; Score 98; DB 1; Length 249;
Best Local Similarity 25.6%; Pred. No. 0.0049;
Matches 23; Conservative 12; Mismatches 27; Indels 28; Gaps 4;

QY 1 CSONEYFDSLLHACIPCOLRCSSNTPLTCQRYCCEYFDSLLHACPLRCSPPTCCYCCF 60
DB 6 CPHQVWDSRRKSCVSCALTCQRS-----QRTCTDF-----CKFINCKRKE----- 46
QY 61 HSEYFDSLLHAC-----PPATCPQYVC 81
DB 47 QGRYDHLHACVSCDSTCTQHPPQCAHFC 76

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RESULT 4
T13X_HUMAN STANDARD; PRT; 293 AA.
ID 113X_HUMAN
AC 014836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 113X_HUMAN
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily."
RL Science 278:138-141(1997).
RN 113X_HUMAN
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN 113X_HUMAN
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bresette D., Carrell J.A., Kaufman T., Peng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinkler D., Lafleur D.,
RA Mignone T.S., Nardelli B., Wei P., Ruben S.M., Ulrich S.J.;
RA Olsen H.S., Kanakaris P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BLYS."
RL J. Biol. Chem. 275:35478-35485(2000).
RN 113X_HUMAN
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delany J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornu M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarsol I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity."
RL Nat. Immunol. 1:252-256(2000).
RN 113X_HUMAN
RP FUNCTION.
RX MEDLINE=9115951; PubMed=1703541;
RA McKinnon P.J., Powell B.C., Rogers G.E.;
RT "Structure and expression of genes for a class of cysteine-rich
RT proteins of the cuticle layers of differentiating wool and hair
RT follicles."
RL J. Cell Biol. 111:2587-2600(1990).
RN 113X_HUMAN
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Aurio J., Gerst C., Bernard B.A., Egly J.-M.;
RT "Genomic organization and promoter characterization of two human UHS
RT keratin genes."
RL Gene 227:137-148(1999).
RN 113X_HUMAN
RP FUNCTION. THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 kDa).
CC TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -1- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.

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DR InterPro; IPR001368; TNFR_c6.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PSS0050; TNFR_NGFR_2; FALSE NEG.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Repeat.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT TRANSMEM 166 186 (POTENTIAL).
FT DOMAIN 187 293 CYTOPLASMIC (POTENTIAL).
FT REPEAT 33 67 TNFR-CYS 1.
FT REPEAT 70 104 TNFR-CYS 2.
FT DISULFID 34 47 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT CONFLICT 251 251 P -> L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 18.7%; Score 93; DB 1; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.017;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

QY 1 CSQNEVPSDLHACIPOLRCSSNTPLTCORC-----EYFDSLHACPLRCS 51
DB 34 CPSEQYMDPLGTGCMCKTICNHQS--QRTCAFCRSLSCRKEGKRYDHLR--DCISCA 90
QY 52 -----PPTCOYCC 59
DB 91 SICQHPKQCAVFC 104

RESULT 5
KRUQ_HUMAN STANDARD; PRT; 169 AA.
ID KRUQ_HUMAN
AC P26371;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
DE KERA).
GN KRN1 OR UHSK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 113X_HUMAN
RP SEQUENCE FROM N.A.
RC TISSUE=Follicle;
RX MEDLINE=9115951; PubMed=1703541;
RA McKinnon P.J., Powell B.C., Rogers G.E.;
RT "Structure and expression of genes for a class of cysteine-rich
RT proteins of the cuticle layers of differentiating wool and hair
RT follicles."
RL J. Cell Biol. 111:2587-2600(1990).
RN 113X_HUMAN
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Aurio J., Gerst C., Bernard B.A., Egly J.-M.;
RT "Genomic organization and promoter characterization of two human UHS
RT keratin genes."
RL Gene 227:137-148(1999).
RN 113X_HUMAN
RP FUNCTION. THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 kDa).
CC TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -1- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.

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us-09-855-158-13.rsp

Tue Jan 7 10:36:48 2003

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CC -!- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC RICH (SR) REPEATS.
CC -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X55293; CAA39005.1; -.
CC DR EMBL; AJ006692; CAA07188.1; -.
CC DR HSSP; P01064; LPI2.
CC DR Genew; HGNC:6409; KRNL.
CC DR MIM; 148021; -.
CC KW Keratin; Repeat; Multigene family.
CC SQ SEQUENCE 169 AA; 16276 MW; 219B14FEB49D4AB CRC64;

Query Match 18.6%; Score 92.5; DB 1; Length 169;
Best Local Similarity 30.0%; Pred. No. 0.012;
Matches 2; Conservative

QY 1 CSQNEYFDSLLHACIPCOLRCSSNTPLTCQRYCCYFVDSLLHAC-PCRLR-----CS 51
DB 77 CSQ-----CSCCKPC-CSSGCGSSCCQCKPCYSCGSCCKPCCSSGRGSSCCQ 127
QY 52 PPTQYCCFHSEYFDSLLHACPPATCPYC 81
DB 128 SSCCKPCCSSGCGSS---CCQSCCKPCC 154

RESULT 6
KRUB HUMAN
ID KRUB_HUMAN STANDARD; PRT; 194 AA.
AC O75690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein B (UHS keratin B) (UHS
DE Krb).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Aurio J., Gerst C., Bernard B.A., Egly J.-M.;
RA "Genomic organization and promoter characterization of two human UHS
RA keratin genes."
RT Gene 227;137-148(1999).
CC -!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS, (40-56 kDa).
CC -!- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -!- DOMAIN MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC RICH (SR) REPEATS.
CC -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
CC -----
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DR EMBL; AJ006692; CAA07188.1; -.
DR HSSP; P01055; 1BBI.
KW Keratin; Repeat; Multigene family.
SQ SEQUENCE 194 AA; 18094 MW; 8607B2AE906FE44A CRC64;

Query Match 18.3%; Score 91; DB 1; Length 194;
Best Local Similarity 31.7%; Pred. No. 0.019;
Matches 26; Conservative

QY 1 CSQNEYFDSLLHACIPCOLRCSSNTPLTCQRYCCYFVDSLLHACPCRLRCSPTT-CQYCC 59
DB 121 CSQSS-----CCKPCS-CSSGCGSSCCQSCCK-----PC-CSQSSCKPCC 160
QY 60 FHSEYFDSLLHACPPATCPYC 81
DB 161 CSQSGCGSS---CCQSCCKPCC 179

RESULT 7
FUR2_DROME
ID FUR2_DROME STANDARD; PRT; 1680 AA.
AC F30432;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
DE FUR2.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
OX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=92381036; PubMed=1512259;
RA Roelcke A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RA Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
RA "Cloning and functional expression of Dfurin2, a subtilisin-like
RA proprotein processing enzyme of Drosophila melanogaster with multiple
RA repeats of a cysteine motif."
RL J. Biol. Chem. 267;17208-17215(1992).
CC -!- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBQUITOUS ENDOPEPTIDASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC CC
CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
CC propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
CC complement component C3 and von Willebrand factor from their
CC respective precursors.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
CC -----
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CC -----
CC EMBL; M94375; AAA28551.1; -.
CC DR EMBL; A43434; A43434.
CC DR HSSP; Q39405; 1MPT.
CC DR MEROPS; S08.049; Fur2.
CC DR FlyBase; FBgn004598; Fur2.
CC DR InterPro; IPR000561; EGF-like.
CC DR InterPro; IPR002174; Furin-like.
CC DR InterPro; IPR002884; P-domain.
CC DR InterPro; IPR000209; Peptidase_S8.
CC DR Pfam; PF00082; Peptidase_S8; 1.
CC DR Pfam; PF01483; P; PARTIAL.
CC DR PRINTS; PR00723; SUBTILISIN.
CC DR ProDom; PD000717; P-domain; 1.
CC DR SMART; SM00181; EGF; 1.

```

SMART: SM00261; FU: 10.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydroxylase, Serine protease, Glycoprotein, Signal, Transmembrane;
KM Multigene family, Zymogen, Repeat
FT SIGNAL 1
FT PROPEP 1 319
FT CHAIN 320 1680
FT ACT_SITE 418 418
FT ACT_SITE 457 457
FT ACT_SITE 638 638
FT DOMAIN 962 1444
FT REPEAT 962 1007
FT REPEAT 1008 1057
FT REPEAT 1058 1104
FT REPEAT 1105 1153
FT REPEAT 1154 1205
FT REPEAT 1206 1254
FT REPEAT 1255 1299
FT REPEAT 1300 1346
FT REPEAT 1347 1393
FT REPEAT 1394 1444
FT TRANSMEM 1508 1532
FT DOMAIN 1533 1680
FT CARBOHYD 3
FT CARBOHYD 109 109
FT CARBOHYD 130 130
FT CARBOHYD 203 203
FT CARBOHYD 443 443
FT CARBOHYD 481 481
FT CARBOHYD 928 928
FT CARBOHYD 1061 1061
FT CARBOHYD 1182 1182
FT CARBOHYD 1275 1275
FT CARBOHYD 1278 1278
FT CARBOHYD 1440 1440
FT SEQUENCE 1680 AA; 18359 MW; 0A99CE8770A8E293 CRC64;

Query Match 17.5%; Score 87; DB 1; Length 1680;
Best Local Similarity 25.0%; Pred. No. 0.3; Matches 31; Mismatches 12; Gaps 50;
Query 1 CSQNEVFDLSLHACIPQQLRCSSTNPPLTQC---RYC-CBYFSLH-----ACP-- 46
Db 1051 CPDGFENSRNKTCTVPCPEPNCAS-----CDHPKCYTSCDH-HLVMEHKVCYSACPDLDT 1103
QY 47 -----CLRCSPPTQCYC--CFHSEYF--DSLHACPPA-----TC 77
Db 1104 YETEDNKCACFCHSTCATCNGPTDODICTCRSSRYAMONKCLISCPDGFYADKRLKCMPC 1163
QY 78 QPYC 81
Db 1164 QEGC 1167

RESULT 8
PCKS_MOUSE
ID_PCKS_MOUSE STANDARD; PRT: 1877 AA.
AC 004557; 062040; 1
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE (Protein convertase subunit)in/lexin type 5 precursor (EC 3.4.21.-)
DE (Protein convertase PCS) (Subtilisin/lexin-like protease PCS)
DE (Convertase PCS) (PC6) (Subtilisin-like protein convertase 6)
DE (SPC6).
GN PCSK5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]

SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB)
RC STRAIN-ICR; TISSUE=Intestine;
RX MEDLINE=93327934; Pubmed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
RT of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171 (1993).
[2]
RT "Identification and functional expression of a new member of the
RT mammalian Kex2-like processing endoprotease family: its striking
RT structural similarity to PACE4.";
RL J. Biochem. 113:132-135 (1993).
[3]
RN SEQUENCE FROM N.A. (ISOFORM PCSA).
RP TISSUE=Adrenal cortex;
RX MEDLINE=93342056; Pubmed=8341687;
RA Lussan J., Vleau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
RT "CNA structure of the mouse and rat subtilisin/kexin-like PCs: a
RT candidate proprotein convertase expressed in endocrine and
RT nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695 (1993).
[4]
RN PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RP MEDLINE=97103178; Pubmed=8947550;
RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
RA Bendayan M., Seidah N.G.;
RT "The isoforms of proprotein convertase PC5 are sorted to different
RT subcellular compartments.";
RL J. Cell Biol. 135:1261-1275 (1996).
[5]
RN DEVELOPMENTAL EXPRESSION.
RP MEDLINE=86293359; Pubmed=8698813;
RX Constant D.B., Calton M., Robertson E.J.;
RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
RT morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191 (1996).
[6]
RN DEVELOPMENTAL EXPRESSION.
RP MEDLINE=97463919; Pubmed=9291583;
RX Rancourt S.L., Rancourt D.E.;
RT "Murine subisin-like proteinase SPC6 is expressed during embryonic
RT implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81 (1997).
-1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
CC OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
CC FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
CC IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
CC OF GROWTH FACTORS.
-1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR IYS.
-1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
CC SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
CC EARLY ENDOSOMES.
-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PCSB/LONG (SHOWN HERE)
CC AND PCSA/SHORT. ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
CC ABUNDANT IN THE INTESITINE AND ADRENALS. PCSB IS EXPRESSED IN THE
CC INTESTINS, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
-1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
CC EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
CC E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
CC E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, ANIONIC AND
CC NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
CC SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN


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DB 72 CRPTCCPTSCQAVGRCPCWATTCQPVSVCCPCRCPTSCOP 114
RESULT 10
UBPM_MOUSE
ID UBPM_MOUSE STANDARD: PRT: 526 AA.
AC 061068;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase DUB-1 (EC 3.1.2.15) (Ubiquitin
thiolesterase DUB-1) (Ubiquitin-specific processing protease DUB-1)
DE (Deubiquitinating enzyme 1).
GN DUB1 OR DUB-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96194957; PubMed:8622927;
RA Zhu Y., Carroll M., Papa F.R., Hochstrasser M., D'Andrea A.D.;
RT "DUB-1, a deubiquitinating enzyme with growth-suppressing activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3275-3279(1996).
CC - FUNCTION: HAS GROWTH-SUPPRESSING ACTIVITY, INDUCES ARREST IN G1
CC - PHASE UPON CONTROLLED EXPRESSION.
CC - CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol
CC - INDUCTION: BY INTERLEUKIN-3
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
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CC EMBL: U41636; AAC52532.1; -
CC DR EMBOPS: C19.031; -
CC DR MEROPS: C19.031; DUB1.
CC DR MGD: MGI:107699; DUB1.
CC DR InterPro: IPR001394; UCH-2.
CC DR Pfam: PF00442; UCH-1; 1.
CC DR Pfam: PF00443; UCH-2; 1.
CC DR PROSITE: PS00972; UCH_2_1; 1.
CC DR PROSITE: PS00973; UCH_2_2; 1.
CC DR PROSITE: PS00973; UCH_2_3; 1.
CC DR Ubl conjugation pathway; Hydrolyase; Thiol protease; Multigene family.
CC FT ACT_SITE 60
CC FT ACT_SITE 288
CC FT ACT_SITE 307
CC FT ACT_SITE 307 BY SIMILARITY.
CC SQ SEQUENCE 526 AA; 59073 MW; 263AAV7579694EA CRC64;
Query Match 16.5%; Score 82; DB 1; Length 526;
Best Local Similarity 35.8%; Pred. No. 0.33;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;
OY 19 LRCSNTPPLTCQRCYCEYFDSLHACPLRCSPPTQYCCFRSEYFDSLH 71
DB 66 LQCLTHTPPV-----ADYWLISOEHSOTC--CSPECKKLCAWEALVTOSILHS 110
RESULT 11
LMG3_HUMAN
ID LMG3_HUMAN STANDARD: PRT: 1587 AA.
AC 09Y6N6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin gamma-3 chain precursor (laminin 12 gamma 3).
GN LMG3.
OS Homo sapiens (Human).
-----
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:98242614; PubMed:10225960;
RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,
RT "Characterization and expression of the laminin gamma3 chain: a novel,
RT non-basement membrane-associated, laminin chain.";
RL J. Cell Biol. 145:605-618(1999).
CC - FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC - SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.
CC - SUBCELLULAR LOCATION: Extracellular.
CC - TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and
CC the reproductive tracts.
CC - DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC - DOMAIN: DOMAIN IV IS GLOBULAR.
CC - SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC - SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAINS.
CC - SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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CC EMBL: AF041835; AAD36991.1; -
CC DR HSSP: P02468; LTEL.
CC DR Genew: HGNC:6494; LAMC3.
CC DR MIM: 604349; -
CC DR InterPro: IPR000561; EGF-like.
CC DR InterPro: IPR001886; LamN.
CC DR InterPro: IPR000034; Laminin B.
CC DR InterPro: IPR002049; Laminin_BGF.
CC DR Pfam: PF00052; laminin_B_1_EGF.
CC DR Pfam: PF00053; laminin_EGF_10.
CC DR Pfam: PF00055; laminin_Nterm_1.
CC DR PRINTS: PRO0011; BGF_LAMININ.
CC DR PRINTS: PD002082; LamN1; 1.
CC DR Pfam: PF003031; Laminin_B_1.
CC DR SMART: SM00180; EGF_Lam_10.
CC DR SMART: SM00001; EGF_Like_1.
CC DR SMART: SM00281; Lamb; 1.
CC DR SMART: SM00136; LamN1; 1.
CC DR PROSITE: PS00022; EGF_1; 7.
CC DR PROSITE: PS01186; EGF_2; 2.
CC DR PROSITE: PS01248; LAMININ_TYPE_EGF; 10.
CC KM Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
CC KM Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
CC FT SIGNAL 19
CC FT CHAIN 20
CC FT CHAIN 1587
CC FT DOMAIN 20
CC FT DOMAIN 270
CC FT DOMAIN 271
CC FT DOMAIN 326
CC FT DOMAIN 327
CC FT DOMAIN 382
CC FT DOMAIN 383
CC FT DOMAIN 429
CC FT DOMAIN 430
CC FT DOMAIN 479
CC FT DOMAIN 480
CC FT DOMAIN 489
CC FT DOMAIN 672
CC FT DOMAIN 490
CC FT DOMAIN 673
CC FT DOMAIN 706
CC LAMININ GAMMA-3 CHAIN.
CC LAMININ N-TERMINAL (DOMAIN VI).
CC LAMININ EGF-LIKE 1.
CC LAMININ EGF-LIKE 2.
CC LAMININ EGF-LIKE 3.
CC LAMININ EGF-LIKE 4.
CC LAMININ EGF-LIKE 5 (N-TERMINAL).
CC LAMININ DOMAIN IV.
CC LAMININ EGF-LIKE 5 (C-TERMINAL).

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FT DOMAIN 707 754 LAMININ EGF-LIKE 6.
FT DOMAIN 755 809 LAMININ EGF-LIKE 7.
FT DOMAIN 810 865 LAMININ EGF-LIKE 8.
FT DOMAIN 866 916 LAMININ EGF-LIKE 9.
FT DOMAIN 917 964 LAMININ EGF-LIKE 10.
FT DOMAIN 965 1013 LAMININ EGF-LIKE 11.
FT DOMAIN 1014 1587 DOMAIN II AND I.
FT DOMAIN 1071 1141 COILED COIL (POTENTIAL).
FT DOMAIN 1200 1229 COILED COIL (POTENTIAL).
FT DOMAIN 1424 1504 COILED COIL (POTENTIAL).
FT SITE 1535 1579 COILED COIL (POTENTIAL).
FT SITE 1587 1597 CELL ATTACHMENT SITE (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 837 837 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 980 980 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 1185 1185 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 1518 1518 N-LINKED (GLCNAC . . .) (POTENTIAL).
SQ SEQUENCE 1587 AA; 172051 MW; 3CB6E09B5F203319 CRC64;

Query Match 16.3%; Score 81; DB 1; Length 1587;
Best Local Similarity 31.0%; Pred. No. 1.1;
Matches 22; Conservative 8; Mismatches 31; Indels 10; Gaps 4;

QY 12 HACPCCQLRCSNTPPLTCQRYCCYFDSLHACPLRC-----SPTCQYCFHSEYFDS 67
DB 322 HECLPC--NCSGRSECTFDR--ELFRSTGHRCHCRDHTAGHCHRCQENFYHMDP 376

QY 68 LLHACPPATCQ 78
DB 377 RM-PQPCDCQ 386

RESULT 12
ID PAC4 RAT STANDARD; PRT; 937 AA.
AC Q63415;1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-)
DE (Subtilisin/kexin-like protease FACE4) (Subtilisin-like proprotein
DE convertase 4) (GPC4).
GN PACE4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Pituitary;
RX MEDLINE=94349873; PubMed=8070361;
RA Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.B.;
RT "PACE4: a subtilisin-like endoprotease prevalent in the anterior
pituitary and regulated by thyroid status";
RL Endocrinology 135:1178-1185(1994).
CC -1- FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTIDASE ACTIVITY WITHIN THE
CC CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
CC DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
CC AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS,
CC WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC COFACTOR: PROBABLY CALCIUM-DEPENDENT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE ANTERIOR PITUITARY AND
CC IN SEVERAL BRAIN REGIONS, THE ATRIUM, AND THE VENTRICLE.
CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
CC ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
CC RETICULUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.

CC CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC EMBL; L31894; AAA61987.1; --
DR HSP; Q99405; IMPT.
DR MEROPS; S08.075; --
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR002884; P domain.
DR InterPro; IPR002029; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF01483; P; PARTIAL.
DR PRINTS; PRO0723; SUBTILISIN.
DR ProDom; PD000717; P domain; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00261; FU; 5.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium;
KW Cleavage on pair of basic residues; Repeat.
FT SIGNAL 46 132 POTENTIAL.
FT PROPEP 46 132 POTENTIAL.
FT CHAIN 133 937 PAIRED BASIC AMINO ACID CLEAVING ENZYME
FT CATALYTIC.
FT DOMAIN 133 454
FT DOMAIN 477 615 HOMO B.
FT DOMAIN 680 937 CYS-RICH MOTIF (CRM) REGION.
FT SITE 132 133 CLEAVAGE (AUTO-).
FT SITE 534 536 CELL ATTACHMENT SITE (POTENTIAL).
FT ACT_SITE 166 196 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 227 227 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 401 401 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 240 240 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 882 882 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 900 900 N-LINKED (GLCNAC . . .) (POTENTIAL).
SQ SEQUENCE 937 AA; 104053 MW; F3865557C33705C8 CRC64;

Query Match 16.2%; Score 80.5; DB 1; Length 937;
Best Local Similarity 24.4%; Pred. No. 0.76; 39; Indels 45; Gaps 6;
Matches 30; Conservative 9; Mismatches 39;

QY 1 CSQNEYFDSLHACIPCLRC-----SNTPLTCOR--YCCYFDSLHACP----- 46
DB 701 CPLGVFGDTARRCRRCHKGCETCTGRSPQCLSCRRGFYHGHQETNCTVLCPLAGLYADE 760

QY 47 ----CLRCSPPTCQY-----CFHSEYFDSLHACPPATCQ 78
DB 761 SORLCLRCH-PSQCKVDEBEKSTVCKEGLARGSCIPDCPEPTVDFSELIRC--GECH 817

QY 79 PVC 81
DB 818 HTC 820

RESULT 13
ID LME2 HUMAN STANDARD; PRT; 1798 AA.
AC P55268; Q16321; Created
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (Laminin B1s chain).
GN LAMB2 OR LAMB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI TaxID=9606;
 RX SEQUENCE FROM N.A.
 MEDLINE=95213013; PubMed=7698745;
 RA Mewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,
 RA Champlaud M.P., Burgess R.E., Albrechtsen R.;
 RT "human beta 2 chain of laminin (formerly S chain): cDNA cloning,
 RT chromosomal localization, and expression in carcinomae";
 RL Genomics 24:243-252(1994).
 RN [3]
 RE SEQUENCE FROM N.A.
 RX MEDLINE=55316263; PubMed=7795887;
 RA Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
 RA Sariola H., Tryggvason K.;
 RT "The human laminin beta 2 chain (S-laminin): structure, expression in
 RT fetal tissues and chromosomal assignment of the LAMB2 gene";
 RL Matrix Biol. 14:489-497(1995).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 CC COMPONENT) S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
 CC CLEFT OF THE NEUROMUSCULAR JUNCTION.
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
 CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
 CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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 CC -----
 DR EMBL; Z68155; CA932279.1; -;
 DR EMBL; Z68156; CA932279.1; JOINED.
 DR EMBL; X79683; CA56130.1; -;
 DR EMBL; X77512; AB34682.2; -;
 DR HSSP; P02468; IKLO.
 DR Genew; HGNC:6487; LAMB2.
 DR MIM; 150325; -;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001886; Lamnt.
 DR InterPro; IPR002049; Laminin_EGF.
 DR Pfam; PF00053; laminin_EGF_13.
 DR Pfam; PF00055; laminin_Nterm_1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD002082; Lamnt; 1.
 DR SMART; SM00180; EGF_Lam; 11.
 DR SMART; SM00136; Lamnt; 1.
 DR PROSITE; PS00023; EGF_1; 10.
 DR PROSITE; PS00186; EGF_2; 2.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 1798 LAMININ BETA-2 CHAIN.
 FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).
 FT DOMAIN 283 346 LAMININ EGF-LIKE 1.

FT DOMAIN 347 409 LAMININ EGF-LIKE 2.
 FT DOMAIN 410 469 LAMININ EGF-LIKE 3.
 FT DOMAIN 521 521 LAMININ EGF-LIKE 4.
 FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).
 FT DOMAIN 553 781 LAMININ EGF-LIKE 6.
 FT DOMAIN 783 830 LAMININ EGF-LIKE 7.
 FT DOMAIN 831 876 LAMININ EGF-LIKE 8.
 FT DOMAIN 877 926 LAMININ EGF-LIKE 9.
 FT DOMAIN 927 985 LAMININ EGF-LIKE 10.
 FT DOMAIN 986 1037 LAMININ EGF-LIKE 11.
 FT DOMAIN 1038 1094 LAMININ EGF-LIKE 12.
 FT DOMAIN 1095 1142 LAMININ EGF-LIKE 13.
 FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
 FT DOMAIN 1190 1409 LAMININ EGF-LIKE 13.
 FT DOMAIN 1410 1442 LAMININ EGF-LIKE 13.
 FT DOMAIN 1443 1798 LAMININ EGF-LIKE 13.
 FT DOMAIN 1453 1526 LAMININ EGF-LIKE 13.
 FT DOMAIN 1472 1790 LAMININ EGF-LIKE 13.
 FT DOMAIN 1577 1790 LAMININ EGF-LIKE 13.
 FT DOMAIN 283 292 LAMININ EGF-LIKE 13.
 FT DISULFID 285 310 LAMININ EGF-LIKE 13.
 FT DISULFID 312 321 LAMININ EGF-LIKE 13.
 FT DISULFID 324 344 LAMININ EGF-LIKE 13.
 FT DISULFID 347 356 LAMININ EGF-LIKE 13.
 FT DISULFID 349 374 LAMININ EGF-LIKE 13.
 FT DISULFID 377 386 LAMININ EGF-LIKE 13.
 FT DISULFID 389 407 LAMININ EGF-LIKE 13.
 FT DISULFID 410 423 LAMININ EGF-LIKE 13.
 FT DISULFID 412 438 LAMININ EGF-LIKE 13.
 FT DISULFID 440 449 LAMININ EGF-LIKE 13.
 FT DISULFID 452 467 LAMININ EGF-LIKE 13.
 FT DISULFID 470 484 LAMININ EGF-LIKE 13.
 FT DISULFID 472 491 LAMININ EGF-LIKE 13.
 FT DISULFID 493 502 LAMININ EGF-LIKE 13.
 FT DISULFID 505 519 LAMININ EGF-LIKE 13.
 FT DISULFID 519 521 LAMININ EGF-LIKE 13.
 FT DISULFID 783 795 LAMININ EGF-LIKE 13.
 FT DISULFID 785 802 LAMININ EGF-LIKE 13.
 FT DISULFID 804 813 LAMININ EGF-LIKE 13.
 FT DISULFID 816 828 LAMININ EGF-LIKE 13.
 FT DISULFID 831 850 LAMININ EGF-LIKE 13.
 FT DISULFID 852 861 LAMININ EGF-LIKE 13.
 FT DISULFID 864 874 LAMININ EGF-LIKE 13.
 FT DISULFID 877 886 LAMININ EGF-LIKE 13.
 FT DISULFID 879 893 LAMININ EGF-LIKE 13.
 FT DISULFID 896 905 LAMININ EGF-LIKE 13.
 FT DISULFID 908 924 LAMININ EGF-LIKE 13.
 FT DISULFID 927 943 LAMININ EGF-LIKE 13.
 FT DISULFID 929 954 LAMININ EGF-LIKE 13.
 FT DISULFID 956 965 LAMININ EGF-LIKE 13.
 FT DISULFID 968 983 LAMININ EGF-LIKE 13.
 FT DISULFID 986 1000 LAMININ EGF-LIKE 13.
 FT DISULFID 988 1007 LAMININ EGF-LIKE 13.
 FT DISULFID 1010 1019 LAMININ EGF-LIKE 13.
 FT DISULFID 1022 1035 LAMININ EGF-LIKE 13.
 FT DISULFID 1095 1107 LAMININ EGF-LIKE 13.
 FT DISULFID 1097 1114 LAMININ EGF-LIKE 13.
 FT DISULFID 1116 1125 LAMININ EGF-LIKE 13.
 FT DISULFID 1128 1140 LAMININ EGF-LIKE 13.
 FT DISULFID 1143 1155 LAMININ EGF-LIKE 13.
 FT DISULFID 1145 1162 LAMININ EGF-LIKE 13.
 FT DISULFID 1164 1173 LAMININ EGF-LIKE 13.
 FT DISULFID 1176 1187 LAMININ EGF-LIKE 13.
 FT DISULFID 1190 1199 LAMININ EGF-LIKE 13.
 FT DISULFID 1193 1193 LAMININ EGF-LIKE 13.
 FT DISULFID 1797 1797 LAMININ EGF-LIKE 13.
 FT CARBOHYD 248 248 LAMININ EGF-LIKE 13.
 FT CARBOHYD 368 368 LAMININ EGF-LIKE 13.
 FT CARBOHYD 1085 1085 LAMININ EGF-LIKE 13.
 FT CARBOHYD 1249 1249 LAMININ EGF-LIKE 13.
 FT CARBOHYD 1348 1348 LAMININ EGF-LIKE 13.
 FT CARBOHYD 1499 1499 LAMININ EGF-LIKE 13.

us-09-855-158-13-rsp

Tue Jan 7 10:36:48 2003

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FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B4890CB7 CRC64;

Query Match
Best Local Similarity 16.2%; Score 80.5; DB 1; Length 1798;
Matches 29; Conservative 7; Mismatches 31; Indels 41; Gaps 8;

QY 1 CSQNEYFDSL-----HACIP-----COL-RCSNPPPTTCQRYCC 35
DQ 943 CHQDEYSQIVCHCRAGYGLRCEACPHFGDPSRPGRCOLCEGNDPMDPD--AC 1000
DY 36 EYFDSLHACPCILRC-----SPPTCQVC--CFHSEYFDSLHACPPATC 77
DQ 1001 D-----PHTGQCLRLHHTGEGPHCAHCKFGFHQAARSHRC---TC 1040

RESULT 14
ID LAM1 HUMAN STANDARD; PRT: 3075 AA.
AC P2539; 1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 41, Last annotation update)
DE 15-JUN-2002 (Rel. 41, Last sequence update)
DE Laminin alpha-1 chain precursor (Laminin A chain).
GN LAM1 OR LAMA (Human)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=91264789; PubMed=1714537;
RX MEDLINE=9133420; PubMed=2733383;
RA Haaparanta T., Uitto J., Ruoslahti E., Engvall E.;
RT "Molecular cloning of the cDNA encoding human laminin A chain.";
RL Matrix 11:151-160(1991).
RN [2]
RP MEDLINE=91264789; PubMed=2049067;
RX MEDLINE=91264789; PubMed=2049067;
RA Nissinen M., Vuolteenaho R., Boot-Handford R., Kallunki P.,
RA Tryggsaasen K.;
RT "Primary structure of the human laminin A chain. Limited expression
RT in human tissues.";
RL Biochem. J. 276:369-379(1991).
RN [3]
RP SEQUENCE OF 1-2628 FROM N.A.
RX MEDLINE=89280632; PubMed=2733383;
RA Olsen D., Nagayoshi T., Fazio M., Peltonen J., Jaakkola S.,
RA Sanborn D., Sasaki T., Kuivaniemi H., Chu M.L., Deutzmann R.,
RA Timpl R., Uitto J.;
RT "Human laminin: cloning and sequence analysis of cDNAs encoding A, B1
RT and B2 chains, and expression of the corresponding genes in human
RT skin and cultured cells.";
RL Lab. Invest. 60:772-782(1989).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND
CC LAMININ-3 (S-LAMININ).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

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CC CC -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC CC -----
CC CC EMBL; X58531; CAA41418.1; -.
CC CC PIR; S14458; 1QOU.
CC CC HSSP; Q60675; 1QOU.
CC CC Genew; HGNC:6481; LAM1.
CC CC MIM; 150320; -.
CC CC InterPro; IPR000561; EGF-like.
CC CC InterPro; IPR001886; LamNT.
CC CC InterPro; IPR000034; Laminin_B.
CC CC InterPro; IPR002049; Laminin_EGF.
CC CC InterPro; IPR001791; Laminin_G.
CC CC Pfam; PF000052; laminin B; 2.
CC CC Pfam; PF000053; laminin EGF; 15.
CC CC Pfam; PF000054; laminin G; 5.
CC CC Pfam; PF000055; laminin Nterm; 1.
CC CC PRINTS; PR00011; EGF-LAMININ.
CC CC ProDom; PD002082; LamNT; 1.
CC CC ProDom; PD003031; Laminin_B; 2.
CC CC SMART; SM00180; EGF Lam; 14.
CC CC SMART; SM00281; EGF-like; 1.
CC CC SMART; SM00282; LamB; 2.
CC CC SMART; SM00282; LamG; 5.
CC CC SMART; SM00136; LamNT; 1.
CC CC PROSITE; PS00022; EGF_1; 11.
CC CC PROSITE; PS01186; EGF_2; 2.
CC CC PROSITE; PS01248; LAMININ TYPE EGF; 15.
CC CC PROSITE; PS50025; LAM G DOMAIN; 5.
CC CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
CC CC SIGNAL 1 17
CC CC CHAIN 18 3075 LAMININ ALPHA-1 CHAIN.
CC CC DOMAIN 18 269 LAMININ N-TERMINAL (DOMAIN VI).
CC CC DOMAIN 270 326 LAMININ EGF-LIKE 1.
CC CC DOMAIN 327 396 LAMININ EGF-LIKE 2.
CC CC DOMAIN 397 453 LAMININ EGF-LIKE 3.
CC CC DOMAIN 454 502 LAMININ EGF-LIKE 4.
CC CC DOMAIN 503 512 LAMININ EGF-LIKE 5 (N-TERMINAL).
CC CC DOMAIN 517 708 LAMININ DOMAIN IV 1 (DOMAIN IV B).
CC CC DOMAIN 709 741 LAMININ EGF-LIKE 5 (C-TERMINAL).
CC CC DOMAIN 742 790 LAMININ EGF-LIKE 6.
CC CC DOMAIN 791 848 LAMININ EGF-LIKE 7.
CC CC DOMAIN 849 901 LAMININ EGF-LIKE 8.
CC CC DOMAIN 902 950 LAMININ EGF-LIKE 9.
CC CC DOMAIN 951 997 LAMININ EGF-LIKE 10.
CC CC DOMAIN 998 1043 LAMININ EGF-LIKE 11.
CC CC DOMAIN 1044 1089 LAMININ EGF-LIKE 12.
CC CC DOMAIN 1090 1149 LAMININ EGF-LIKE 13.
CC CC DOMAIN 1150 1159 LAMININ EGF-LIKE 14.
CC CC DOMAIN 1160 1361 LAMININ DOMAIN IV 2 (DOMAIN IV A).
CC CC DOMAIN 1362 1402 LAMININ EGF-LIKE 14 (C-TERMINAL).
CC CC DOMAIN 1403 1451 LAMININ EGF-LIKE 15.
CC CC DOMAIN 1452 1508 LAMININ EGF-LIKE 16.
CC CC DOMAIN 1509 1555 LAMININ EGF-LIKE 17.
CC CC DOMAIN 1556 2116 LAMININ I AND 1.
CC CC DOMAIN 2117 2297 LAMININ G-LIKE 1.
CC CC DOMAIN 2298 2481 LAMININ G-LIKE 2.
CC CC DOMAIN 2482 2673 LAMININ G-LIKE 3.
CC CC DOMAIN 2674 2885 LAMININ G-LIKE 4.
CC CC DOMAIN 2886 3070 LAMININ G-LIKE 5.
CC CC DOMAIN 3071 3796 COILED COIL (POTENTIAL).
CC CC DOMAIN 3797 1706 COILED COIL (POTENTIAL).
CC CC DOMAIN 1968 1989 COILED COIL (POTENTIAL).
CC CC DOMAIN 2088 2120 COILED COIL (POTENTIAL).
CC CC DOMAIN 2534 2536 CELL ATTACHMENT SITE.

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FT DISULFID 270 279 BY SIMILARITY.
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 FT DISULFID 297 305 POTENTIAL.
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 FT DISULFID 772 788 BY SIMILARITY.
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 FT DISULFID 902 914 BY SIMILARITY.
 FT DISULFID 904 921 BY SIMILARITY.
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 FT DISULFID 1007 1007 BY SIMILARITY.
 FT DISULFID 1000 1014 BY SIMILARITY.
 FT DISULFID 1016 1025 BY SIMILARITY.
 FT DISULFID 1028 1041 BY SIMILARITY.
 FT DISULFID 1044 1056 BY SIMILARITY.
 FT DISULFID 1064 1063 BY SIMILARITY.
 FT DISULFID 1065 1074 BY SIMILARITY.
 FT DISULFID 1077 1087 BY SIMILARITY.
 FT DISULFID 1403 1412 BY SIMILARITY.
 FT DISULFID 1405 1419 BY SIMILARITY.
 FT DISULFID 1432 1431 BY SIMILARITY.
 FT DISULFID 1434 1449 BY SIMILARITY.
 FT DISULFID 1452 1466 BY SIMILARITY.
 FT DISULFID 1454 1476 BY SIMILARITY.
 FT DISULFID 1479 1488 BY SIMILARITY.
 FT DISULFID 1481 1506 BY SIMILARITY.
 FT DISULFID 1509 1521 BY SIMILARITY.
 FT DISULFID 1511 1528 BY SIMILARITY.
 FT DISULFID 1530 1539 BY SIMILARITY.
 FT DISULFID 1542 1553 BY SIMILARITY.
 FT DISULFID 1556 1556 BY SIMILARITY.
 FT DISULFID 1560 1560 INTERCHAIN (PROBABLE).
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 555 555 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 763 763 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 926 926 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 952 952 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1407 1407 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1579 1579 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1678 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1689 1689 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1698 1698 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1717 1717 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 16.1%; Score 80; DB 1; Length 3075;
 Best Local Similarity 23.4%; Pred. No. 2.4;
 Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSONEYFSPSL--HACPCO-----LRCSNTPPLTCORCC-- 36
 DB 831 CADGYGNPTVPSSCVPDCSGNVDPSEAGHCDVTSGLCKLGNWDGANCER-CADGF 889
 QY 37 YFDSL---LHACPC-----LRCSP-PTCOYC--CFHSEYFDSLHACP 73
 DB 890 YGDVATKNCACACCHVKSHSAVCHLETLGCLCDCKENVTCGCCDCLHGYGLDSGHCR 949
 QY 74 PATC 77
 DB 950 PCNC 953

RESULT 15
 YNC3_YEAST STANDARD; PRT; 965 AA.
 ID YNC3_YEAST
 AC P53971;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 108.5 kDa protein in UME3-HDA1 intergenic region.
 GN YNL023C OR N2812.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duesterhoeft A., Floeth M., Fritze C., Heuss-Neitzel D.,
 RA Hilbert H., Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Andre B., Itagaki Housaani I., Urrestarazu L.A., Vissers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: TO DROSOPHILA SHUTTLE CRAFT PROTEIN (STC) AND HUMAN
 CC NFX1.
 CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; Z71299; CA95885.1; --
 CC SGD; S0004966; YNL023C.
 DR InterPro; IPR001374; R3H.
 DR InterPro; IPR000967; Znf_NFX1.
 DR InterPro; IPR001841; Znf_Ring.
 DR Pfam; PF01422; Zf-NFX1; 5.
 DR Pfam; PF01424; R3H; 1.
 DR SMART; SM00393; R3H; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; SM00438; Znf_NFX; 7.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00589; ZF_RING_2; 1.
 KW Hypothetical protein; zinc-finger; Repeat.
 FT ZN FING 68 118 RING-TYPE.
 FT DOMAIN 150 644 7 X APPROXIMATE REPEATS, CYS-RICH.
 FT REPEAT 150 185 1.
 FT REPEAT 206 251 2.
 FT REPEAT 273 330 3.
 FT REPEAT 352 390 4.
 FT REPEAT 458 497 5.
 FT REPEAT 575 610 6.

us-09-855-158-13.rsp

Tue Jan 7 10:36:48 2003

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FT REPEAT 611 644 7. 121C57BB07C6FA9D CRC64;  
SQ SEQUENCE 965 AA; 108494 MW; 121C57BB07C6FA9D CRC64;  
Query Match 16.0%; Score 79.5; DB 1; Length 965;  
Best Local Similarity 29.6%; Pred. No. 0.98; 26; Indels 37; Gaps 7;  
Matches 29; Conservative 6; Mismatches 26; Indels 37; Gaps 7;  
QY 12 HACT-PCQLRCSSTPPLTCQRYC-----CEYFDSLHACPC-----LRCSP--P 53  
Db 456 HICLKPCNLTLSCGIH--KCQRKCHPGKCPCLSDSDNLDVCPGNTVVVPAPVRCGTKLP 513  
QY 54 TCQYCCF-----HSEYFDSLHACPPAT 76  
Db 514 TCNHPCKVVRGESCQGHKMPHTCH--SLDVSCPCT 549
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Search completed: January 7, 2003, 09:38:07
Job time : 8.05023 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 22.9398 Seconds
(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEFSLHACIPCLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_podent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	20.2	1792	13	O57484
2	94.5	19.0	223	11	O62220
3	94.5	19.0	230	11	O64507
4	93.5	18.8	195	11	O9D141
5	92.5	18.6	169	4	Q14564
6	92.5	18.6	227	11	O9D225
7	91.5	18.4	136	4	O9BYR5
8	91.5	18.4	186	4	O9BYR2
9	91.5	18.4	186	11	O64526
10	91.5	18.4	191	11	O9D3H7
11	89	17.9	159	4	O88281
12	89	17.9	1574	11	O88281
13	88	17.7	166	4	O9BYR3
14	87.5	17.6	154	4	O9BYQ2
15	87.5	17.6	174	4	O9BYQ4
16	87.5	17.6	193	4	O9BYQ5

17	87	17.5	159	4	O9BYQ0
18	87	17.5	165	11	O9D7P3
19	87	17.5	195	11	O9D0X9
20	87	17.5	1376	5	O8S2S2
21	87	17.5	1673	5	O24301
22	86	17.3	188	11	O70148
23	86	17.3	2112	5	O8WPL0
24	85.5	17.2	154	4	O9BYP9
25	85.5	17.2	177	11	O9D644
26	85.5	17.2	189	11	O9D527
27	85	17.1	202	11	O91W93
28	85	17.1	325	10	O94HS1
29	84.5	17.0	767	13	O9DGR2
30	84	16.9	195	4	O9BYO6
31	84	16.9	201	4	O9BQ66
32	84	16.9	210	4	O9BYR0
33	84	16.9	1671	5	O9NJV5
34	83.5	16.8	110	5	O9BIR2
35	83.5	16.8	130	11	O92287
36	83.5	16.8	191	4	O9BYQ8
37	83	16.7	175	4	O7628
38	82	16.5	98	4	O9BYR8
39	82	16.5	126	6	O28707
40	82	16.5	167	11	O9D122
41	82	16.5	168	11	O9D732
42	81.5	16.4	85	11	O70555
43	81.5	16.4	429	13	O91650
44	81	16.3	353	5	O9VW81
45	81	16.3	353	5	O8S2S8

ALIGNMENTS

RESULT 1

O57484	PRELIMINARY;	PRT; 1792 AA.
ID	O57484	
AC	O57484	
DT	01-JUN-1998 (TRENBLrel. 06, Created)	
DT	01-JUN-1998 (TRENBLrel. 06, Last sequence update)	
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)	
DE	Laminin beta 2-like chain.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=93015947; PubMed=1400373;	
RA	O'Rear J.J.;	
RT	"A novel laminin B1 chain variant in avian eye.";	
RL	J. Biol. Chem. 267:20555-20557(1992).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=98209634; PubMed=9550264;	
RA	Liu J., Swadlow S., Xie W., Brewton R.G., Mayne R.;	
RT	"Primary structure and expression of a chicken laminin beta chain: evidence for four beta chains in birds.";	
RL	Matrix Biol. 16:471-481(1998).	
DR	EMBL; AF038555; AAB92586.1; -.	
DR	HSSP; P02468; ILO.	
DR	InterPro; IPR002106; tRNA ligaseII.	
DR	InterPro; IPR000561; EGF-like.	
DR	InterPro; IPR002049; Laminin_EGF.	
DR	InterPro; IPR001886; LamNT.	
DR	Pfam; PF00053; laminin_EGF; 13.	
DR	Pfam; PF00055; laminin_Nterm; 1.	
DR	PRINTS; PR00011; EGF_LAMININ.	
DR	SMART; SM00180; EGF_Iam; 13.	
DR	SMART; SM00136; LamNT; 1.	
DR	PROSITE; PS00339; AA TRNA LIGASE II_2; UNKNOWN_1.	
DR	PROSITE; PS00022; EGF_1; UNKNOWN_10.	

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
 KW EGF-like domain; Glycoprotein; Laminin EGF-like domain; Repeat.
 SQ SEQUENCE 1792 AA; 195723 MW; 4A4CB0206FA600 CRC64;

Query Match 20.2%; Score 100.5; DB 13; Length 1792;
 Best Local Similarity 32.0%; Pred. No. 0.00059;
 Matches 32; Conservative 8; Mismatches 35; Indels 25; Gaps 6;

QY 1 CSQNEFYDSLHACIPQALRCSSNTPTLC--QRYCCYFDSLHACP-----CLR 49
 DB 1017 CGPGYGDARHSC-----RRCSCNTLTGTDPTNGPQCCQDQSGCHCLPHVEGQSCDR 1072
 QY 50 CSP-----PTQYCCYFDSLHACPPATQPYC 81
 DB 1073 CSPHFMNLGSGGCEPCACHPH--SLSPACNOFTQCCSC 1110

RESULT 2

ID Q62220 PRELIMINARY; PRT; 223 AA.

AC Q62220;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Serine 2 ultra high sulfur protein.
 GN KRTAP5-4.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RN [1]_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C.

RC MEDLINE=91065960; PubMed=2250030;

RA Wood L., Mills M., Hatzenduhler N., Vogel G.,

RT "Serine-rich ultra high sulfur protein gene expression in murine hair

RL and skin during the hair cycle."

RU J. Biol. Chem. 265:21375-21380(1990).

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C.

RC MEDLINE=91154184; PubMed=1840598;

RA Wood L., Mills M., Hatzenduhler N., Vogel G.,

RT "Additions and Corrections: Serine-rich ultra high sulfur protein gene

RL expression in murine hair and skin during the hair cycle."

RU J. Biol. Chem. 266:4024-4024(1991).

DR EMBL; M37760; AAA40107.1; -.

DR HSSP; P01064; IP12.

DR MGD; MG1:1354758; Krtap5-4.

DR InterPro; IPR001450; 4Fe4S_ferredoxin.

DR InterPro; IPR001007; VWF_C.

DR PROSITE; PS00198; 4Fe4S_FERREDOXIN.

DR PROSITE; PS01208; VWF_C; UNKNOWN_2.

SQ SEQUENCE 223 AA; 21442 MW; C65BDB9FPD08C59A CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 223;
 Best Local Similarity 29.6%; Pred. No. 0.00052;

Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQALRCSSNTPTLC--QRYCCYFDSLHACP-----CLR 49
 DB 150 CCQSS-----CCKPC--CQSSGCCSCCQSSCK-----PCC-QQSSCCKPCC 189
 QY 61 HSEYFDSLHACPPATQPYC 81
 DB 190 QSS-----CCKPCCQSSC 203

RESULT 3

ID Q64507 PRELIMINARY; PRT; 230 AA.

AC Q64507;

DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Serine 1 ultra high sulfur protein.
 GN KRTAP5-1.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RN [1]_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C.

RC MEDLINE=91065960; PubMed=2250030;

RA Wood L., Mills M., Hatzenduhler N., Vogel G.,

RT "Serine-rich ultra high sulfur protein gene expression in murine hair

RL and skin during the hair cycle."

RU J. Biol. Chem. 265:21375-21380(1990).

DR EMBL; M37759; AAA40106.1; -.

DR HSSP; P01064; IP12.

DR MGD; MG1:1354732; Krtap5-1.

DR InterPro; IPR001450; 4Fe4S_ferredoxin.

DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR001305; DnaJ_CXXCXXG.

DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.

DR PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.

DR PROSITE; PS00637; DnaJ_CXXCXXG; UNKNOWN_1.

DR PROSITE; PS01208; VWF_C; UNKNOWN_3.

SQ SEQUENCE 230 AA; 21781 MW; 6CC5081B2137C23 CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 230;
 Best Local Similarity 29.6%; Pred. No. 0.00053;
 Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQALRCSSNTPTLC--QRYCCYFDSLHACP-----CLR 49
 DB 149 CCQSS-----CCKPC--CQSSGCCSCCQSSCK-----PCC-QQSSCCKPCC 188
 QY 61 HSEYFDSLHACPPATQPYC 81
 DB 189 QSS-----CCKPCCQSSC 202

RESULT 4

ID Q6D141 PRELIMINARY; PRT; 195 AA.

AC Q6D141;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE 18 days embryo cDNA, RIKEN full-length enriched library,
 DE clone:1110030N11, full insert sequence.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=EMBRIO;

RC MEDLINE=C57BL/6J; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,

RA Aizawa K., Hara A., Fukunishi Y., Kono H., Mauchi J., Fukuda S.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaakawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsumoto Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schmitt L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmam C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ ultrahigh keratin
 RT associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ406934; CAC27573.1; -
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF01500; Keratin_B2; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 SQ SEQUENCE 136 AA; 14402 MW; 51E514863925E02E CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 136;
 Best Local Similarity 29.7%; Pred. No. 0.00079;
 Matches 27; Conservative 5; Mismatches 38; Indels 21; Gaps 5;

QY 10 LILACIP--COLRC-----SNTPLTCQRYCEYFDSLILHAC--PCLR---C 50
 DB 17 LENCCKRPSCCQYTCRTCCRCPSCVSSCCRPCCQSVCCQPTCCSPSCCQTCCTTC 76
 QY 51 SPPTQYCCFHSYFDSLILHACPATQPYC 81
 DB 77 RPSCCVSSCFRPPCCQSV--CCQPTCCRPSC 105

RESULT 8

Q9BYR2 PRELIMINARY; PRT; 186 AA.
 ID Q9BYR2;

AC Q9BYR2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Keratin associated protein 4.5.
 GN KRTAB4.5

OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmam C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ ultrahigh keratin
 RT associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ406937; CAC27576.1; -
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001304; Keratin_C.
 DR InterPro; IPR001368; TNFR_C6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin_B2; 1.
 DR PROSITE; PS00615; C_TYR_LIGAND_1; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_2.
 SQ SEQUENCE 186 AA; 19916 MW; 034D9C7343D4F63A CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 186;
 Best Local Similarity 30.5%; Pred. No. 0.001; 28; Indels 23; Gaps 6;
 Matches 25; Conservative 6; Mismatches 28; Indels 23; Gaps 6;

QY 10 LILACIP--COLRCSSNT--PPLTCQRYCEYFDSLILHACPLRCSPPTC-----QYCC 59
 DB 17 LENCCKRPSCCQYTCRTCCRCPSCVSSCCRPCCQSVCCQPTCCSPSCCQTCCTTC 71
 QY 60 FHSYFDSLILHACPATQPYC 81
 DB 72 ESS-----CCRPPCCRPSC 85

RESULT 9

Q64526

ID Q64526 PRELIMINARY; PRT; 186 AA.
 AC Q64526;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Ultra-high sulphur keratin.
 GN KRTAP9-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=89140394; PubMed=2465353;
 RA McNab A.R., Wood L., Theriault N., Gierman T., Vogel G.;
 RT "An ultra-high sulfur keratin gene is expressed specifically during
 RT hair growth".
 RL J. Invest. Dermatol. 92:263-266(1989).
 CC 1. SIMILARITY: TO THE PLANT THIONIN FAMILY.
 DR EMBL; M27685; AA81560.1; -
 DR MGd; MG1305997; Krtap9-1.
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001010; Thionin.
 DR InterPro; IPR001368; TNFR_C6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin_B2; 1.
 DR PROSITE; PS00271; THIONIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_1.
 SQ SEQUENCE 186 AA; 19658 MW; 61D6BFDAB72CFEB4 CRC64;

Query Match 18.4%; Score 91.5; DB 11; Length 186;
 Best Local Similarity 34.7%; Pred. No. 0.001; 24; Indels 19; Gaps 6;
 Matches 25; Conservative 4; Mismatches 19; Indels 19; Gaps 6;

QY 14 CIP--COLRC--SNTPLTCQRYCEYFDSLILHAC--PCLRSPPTQYCCFHSYFDSLIL 69
 DB 85 CQPCQPSCCQSVCCQPTCCRCPSCVSSCCRPCCQSVCCQPTCCSPSCCQTCCTTC 132
 QY 70 HACPPATQPYC 81
 DB 133 --CRPC--CQPC 141

RESULT 10

Q9D3H7 PRELIMINARY; PRT; 191 AA.
 ID Q9D3H7;

AC Q9D3H7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 10 days neonate head cDNA, RIKEN full-length enriched library,
 DE clone:5530401L02, full insert sequence.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=C57BL/6J; TISSUE=HEAD;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Strahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicich S., Hill D., Hofmann W., Hume D.A., Kamiya M., Lee N.H.,

us-09-855-158-13.ra1

Tue Jan 7 10:36:46 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:14 ; Search time 9.94737 Seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNYFDSLLHACIPCOLR.....SEYFDSLLHACPPATCQPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgm2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgm2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgm2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgm2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgm2_6/ptodata/1/iaa/PCURS COMB.pcp.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	18.7	166	2	US-08-810-572A-6
2	93	18.7	166	4	US-09-290-333-6
3	93	18.7	293	4	US-08-810-572A-2
4	93	18.7	293	4	US-09-290-333-2
5	82	16.5	508	4	US-09-019-095A-8
6	82	16.5	521	4	US-09-019-095A-22
7	82	16.5	526	4	US-09-019-095A-2
8	80	16.1	3075	2	US-08-460-309-5
9	80	16.1	3075	2	US-08-125-077-5
10	80	16.1	5405	4	US-08-718-388-9
11	79	15.9	320	4	US-09-183-861-22
12	79	15.9	320	4	US-09-183-861-55
13	79	15.9	320	4	US-09-023-765-22
14	79	15.9	320	4	US-09-023-765-55
15	79	15.9	545	4	US-09-019-095A-38
16	78	15.7	109	2	US-08-527-044-2
17	78	15.7	109	3	US-09-013-780-2
18	77.5	15.6	139	3	US-08-965-903B-20
19	77.5	15.6	139	4	US-09-370-398-4
20	76.5	15.4	2414	1	US-08-227-536-2
21	76.5	15.4	2414	1	PCP-US95-04682-2
22	76	15.3	2441	1	US-08-861-468-2
23	76	15.3	2441	3	US-08-861-739-2
24	76	15.3	2441	4	US-08-814-247A-8
25	76	15.3	2442	4	US-08-814-247A-10
26	75.5	15.2	156	3	US-08-600-982-30
27	75.5	15.2	156	5	PCP-US94-10261A-30

28	75.5	15.2	1713	3	US-08-600-982-24
29	75.5	15.2	1713	5	PCP-US94-10261A-24
30	75	15.1	219	1	US-08-152-019A-31
31	75	15.1	219	2	US-08-460-309-18
32	75	15.1	219	2	US-08-125-077-18
33	75	15.1	430	3	US-08-397-897-2
34	75	15.1	430	4	US-09-156-836B-2
35	73.5	14.8	435	4	US-09-561-989-10
36	73	14.7	689	4	US-09-177-249-2
37	73	14.7	689	4	US-09-061-769A-2
38	72.5	14.6	969	2	US-08-284-941-2
39	72.5	14.6	969	2	US-08-447-642-2
40	72.5	14.6	969	4	US-09-236-503-2
41	72.5	14.6	969	5	PCP-US93-02147A-2
42	72	14.5	275	1	US-08-312-870-7
43	72	14.5	366	4	US-08-857-076-103
44	72	14.5	446	1	US-08-307-444A-5
45	72	14.5	446	1	US-08-587-389-5

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102

GENERAL INFORMATION:
APPLICANT: Bram, Richard J.

APPLICANT: von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESS: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-FEB-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq. David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-431-1684

TELEFAX: 201-431-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-810-572A-6

Query Match 18.7%; Score 93; DB 2; Length 166;

Best Local Similarity 28.4%; Pred. No. 0.037;

Tue Jan 7 10:36:46 2003

us-09-855-158-13.rai

Page 2

	Matches	2;	Conservative	13;	Mismatches	22;	Indels	18;	Gaps	5;
QY	1	CSONEVPSDLHACIFCOLBGSNTPEPLTCQRVC-----EYPSLLIHACPICRGS	51							
		: :								
Dd	34	CPEQGYNDPLILGCTMCKRTIKNHS-QRTCAAFCSLSLSCREKGGKFYDHLR--DIISCA	90							
QY	52	-----PPTQQYCC	59							
Dd	91	SICGMHPKOCATFC	104							

RESULT 2

US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: DAVID A. JACKSON, JR.;
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor

21P: 07601

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09
FILING DATE: 12-Apr-1999
CLASSIFICATION: ~~Unknown~~

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eric David A

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT

TELEPHONE: 201-487-5
TELEFAX: 201-343-168

SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids

STRANDEDNESS: sin
TOPOLOGY: linear

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; MOLECULE LIFE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
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Query Match	18.7%;	Score 93;	DB 4;	Length 166;
Best Local Similarity	28.4%;	Pred. No. 0.037;		
Matches 21; Conservative	13;	Mismatches 22;	Indels 18;	Gaps 5

RESULT 3
US-08-810-572A-2
: Sequence 2, Application US/08810572A

;; patent No. 5969102
;; GENERAL INFORMATION:
: APPLICANT: Bram, Richard J

APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAM1. NITROIC ACIDS ENCODING THE SAME AN

; TITLE OF INVENTION: THEREOF
 ;
 ; NUMBER OF SEQUENCES: 11
 ;
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: David
STREET: 411 Hack
; ;
STREET: Elcor

CITY: Hackensack
STATE: New Jersey

ZIP: 07601
COMPUTER READABLE FORM:

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE. FACILITY NEEDED
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/0
;

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FILED DATE: 20-FEB-1991
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: JACKSON Esq., DAVID A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-00

TELECOMMUNICATION INFORMATION
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

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; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acid

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: 1:nonc

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MOLECULE TYPE: protein
HYPOTHETICAL: NO

Query Match	18.7%;	Score 93;	DB 2;	Length 293;
Best Local Similarity	28.4%;	Pred. No. 0.064;		
Matches 21; Conservative	13;	Mismatches 22;	Indels 18;	Gaps 5

RESULT 4

; Sequence 2, Application US/0929033
; Patent No. 6316222

APPLICANT: Bram, Richard J.
von Bulow, Goltz

1 TITLE OF INVENTION: A LIMFOCITE SURFACE RECEPTOR THAT BINDS
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NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

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us-09-855-158-13.ra1

Page 4

Query Match 16.5%; Score 82; DB 4; Length 526;
Best Local Similarity 35.8%; Pred. No. 1.2; Indels 8; Gaps 2;
Matches 19; Conservative 8; Mismatches 18;

QY 19 LRCSSNTPPLTCORVCEYFDSLHACPLRCSPPTCOYCFHSEYFDSLHAC 71
DB 66 LQCLHTHPPL-----ADWYLSQEHSTC--CSPECKICAMEALVTGSLHLS 110

RESULT 8

US-08-460-309-5
Sequence 5, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3075 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-5

Query Match 16.1%; Score 80; DB 2; Length 3075;

Best Local Similarity 23.4%; Pred. No. 10;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEVFDLSL--HACIPCO-----LRCSSNTPPLTCORVCE-- 36
DB 831 CADGYGNPTVPBESCVPCDCSGNVDPSEAGHDSVTGECIKLGNTDGAHCR--CADGF 889
QY 37 YFDSL-----LHACPC-----LRCSP--PTCOYC--CFHSEYFDSLHAC 73
DB 890 YGDAVTKNCRACGCHVKSASHAVCHLETLGLCDCKPNVTGQCCDQCLHGYGLDSHGCR 949
QY 74 PATC 77

DB 950 PCNC 953

RESULT 9

US-08-125-077-5
Sequence 5, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3075 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-5

Query Match 16.1%; Score 80; DB 2; Length 3075;

Best Local Similarity 23.4%; Pred. No. 10;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEVFDLSL--HACIPCO-----LRCSSNTPPLTCORVCE-- 36
DB 831 CADGYGNPTVPBESCVPCDCSGNVDPSEAGHDSVTGECIKLGNTDGAHCR--CADGF 889
QY 37 YFDSL-----LHACPC-----LRCSP--PTCOYC--CFHSEYFDSLHAC 73
DB 890 YGDAVTKNCRACGCHVKSASHAVCHLETLGLCDCKPNVTGQCCDQCLHGYGLDSHGCR 949
QY 74 PATC 77
DB 950 PCNC 953

RESULT 10
US-08-718-388-9

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Tue Jan 7 10:36:46 2003

Sequence 9, Application US/08718388
Patent No. 6271362
GENERAL INFORMATION:
APPLICANT: MORIKAWA, MINORU
TITLE OF INVENTION: GENE ENCODING IgG FC REGION-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-388-9

Query Match 16.1%; Score 80; DB 4; Length 5405;
Best Local Similarity 25.4%; Pred. No. 17;
Matches 29; Conservative 12; Mismatches 48; Gaps 10;
QY 1 CSQNEYFDSLHACI-PCQRCSSNTPPLTCQRYCCEYFDSLHACPC-----LRCS 51
DB 2733 CPQNGHYE---LCADTCSLGSALSAPLQCPDCAE-----GCQDSGFLYNGOACV 2781
QY 52 PPTCQVC-CFHS-EYFD---SL-----HACPPA-TCQP 79
DB 2782 P--IQCGCYHNGAYPEPTVLIDNCRCQCTCHAGKVVVQCEHSCKFGQVCQP 2833

RESULT 11
US-09-183-861-22
Sequence 22, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 09/022,765
APPLICATION NUMBER: 12-FEB-1998
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-861-22

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;
QY 13 ACIPCO-----LRCSN---TPPLTCQRYCCEYFDSLHACPCLRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTCAPNYLTPLLTCTSPVAC---NIEH---CMQCDPQT 157
QY 55 --COYCC--PHSEYFDSLH--ACPPATCQ 78
DB 158 SRQECVSPYVDSYDGLCRLSDACSVNCK 188

RESULT 12
US-09-183-861-55
Sequence 55, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 09/022,765
APPLICATION NUMBER: 12-FEB-1998
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-183-861-55

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5; Mismatches 23; Indels 32; Gaps 7;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

OY 13 ACIPQ-----LRCSN--TPPLTCQRYCCYFDSLHACPCIRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPPLTCSPVAC---NIEH---CMQCDPQTP 157
OY 55 --CQYCC--FHSEYFDSLH--ACPPATQ 78
DB 158 SRCQECVSPYVDSYDGLCRISDACSVPNCK 188

RESULT 13
US-09-022-765-22
Sequence 22, Application US/09022765
Patent No. 6375955

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yaser A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-765-22

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5; Mismatches 23; Indels 32; Gaps 7;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

OY 13 ACIPQ-----LRCSN--TPPLTCQRYCCYFDSLHACPCIRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPPLTCSPVAC---NIEH---CMQCDPQTP 157
OY 55 --CQYCC--FHSEYFDSLH--ACPPATQ 78
DB 158 SRCQECVSPYVDSYDGLCRISDACSVPNCK 188

RESULT 14
US-09-022-765-55
Sequence 55, Application US/09022765
Patent No. 6375955

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yaser A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-022-765-55

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5; Mismatches 23; Indels 32; Gaps 7;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

OY 13 ACIPQ-----LRCSN--TPPLTCQRYCCYFDSLHACPCIRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPPLTCSPVAC---NIEH---CMQCDPQTP 157
OY 55 --CQYCC--FHSEYFDSLH--ACPPATQ 78
DB 158 SRCQECVSPYVDSYDGLCRISDACSVPNCK 188

RESULT 15
US-09-019-095A-38

Sequence 38, Application US/09019095A
Patent No. 6287858
GENERAL INFORMATION:
APPLICANT: D'Andrea, Alan D.

us-09-855-158-13.ra1

Tue Jan 7 10:36:46 2003

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; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; TITLE OF INVENTION: Cell Growth
; FILE REFERENCE: DFCI-435p2A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; PRIOR FILING DATE: 1998-02-05
; CURRENT APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 545
; TYPE: PRT
; ORGANISM: murine
; US-09-019-095A-38

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Query Match 15.9%; Score 79; DB 4; Length 545;
Best Local Similarity 34.0%; Pred. No. 2.4;
Matches 18; Conservative 9; Mismatches 18; Indels 8; Gaps 2;

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QY 19 LRCSSNTPLTCQRYCCYCFDLSLLHACPLRCSPPTCQYCCFHFSEYFDSLLHA 71
DB 56 LQCLHTPPL-----ADYMLSQEYSQTC--CSPEGCKMCAMEAHVTQSLLHS 110

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Tue Jan 7 10:36:46 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: January 7, 2003, 09:40:20 ; Search time 6.09023 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEYFDSLHACIPCOLR.....SEYFDSLHACPPATCQPYC 81

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 117078 seqs, 18951520 residues
Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubaa/US05 NEW PUB. pep.*
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10: /cgn2_6/ptodata/1/pubaa/US10 NEW PUB. pep.*
11: /cgn2_6/ptodata/1/pubaa/US10 PUBCOMB. pep.*
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13: /cgn2_6/ptodata/1/pubaa/US60 PUBCOMB. pep.*
14: /cgn2_6/ptodata/1/pubaa/US60 PUBCOMB. pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	498	100.0	81	10	US-09-854-864-13
2	230.5	46.3	207	9	US-10-077-438-3
3	230.5	46.3	207	9	US-10-077-137-3
4	201.5	40.5	283	10	US-09-854-864-9
5	201.5	40.4	283	10	US-09-854-864-7
6	201.4	40.4	51	10	US-09-854-864-6
7	201.4	40.4	58	10	US-09-854-864-21
8	201.4	40.4	181	10	US-09-854-864-5
9	201.4	40.4	184	9	US-10-077-438-1
10	201.4	40.4	184	9	US-10-077-438-7
11	201.4	40.4	184	9	US-10-077-137-1
12	201.4	40.4	184	9	US-10-077-137-7
13	139.5	30.7	117	10	US-09-854-864-12
14	139.5	28.0	281	10	US-09-854-864-10
15	136	27.3	185	10	US-09-854-864-11
16	105	21.1	166	10	US-09-854-864-16
17	93	18.7	166	10	US-09-854-864-15
18	93	18.7	291	9	US-09-779-050A-43
19	93	18.7	293	9	US-09-779-050A-42

93	18.7	293	9	US-10-084-971-2	Sequence 2, Appl
93	18.7	293	10	US-09-879-919-22	Sequence 22, Appl
93	18.7	293	10	US-09-854-864-14	Sequence 14, Appl
93	18.7	293	10	US-09-961-376-2	Sequence 2, Appl
93	18.7	297	10	US-09-854-864-18	Sequence 18, Appl
93	18.7	297	10	US-09-854-864-18	Sequence 37946, A
91.5	18.4	231	10	US-09-864-761-37946	Sequence 145, Appl
89.5	18.0	134	10	US-09-864-761-39564	Sequence 39564, A
84.5	17.0	270	10	US-09-764-855-145	Sequence 46675, A
83	16.7	93	10	US-09-864-761-46675	Sequence 3, Appl
82	16.3	230	10	US-09-874-062-3	Sequence 10, Appl
81	16.3	1587	10	US-09-845-583-10	Sequence 39864, A
80.5	16.2	85	10	US-09-864-761-39864	Sequence 9, Appl
80.5	16.2	1798	10	US-09-938-275-9	Sequence 5, Appl
80	16.1	3075	10	US-09-938-275-5	Sequence 1116, Ap
80	16.1	5405	9	US-10-025-380-1116	Sequence 1116, Ap
80	16.1	5405	10	US-09-922-217-1116	Sequence 20, Appl
79	15.9	59	10	US-09-854-864-20	Sequence 22, Appl
79	15.9	320	9	US-08-991-496-22	Sequence 55, Appl
79	15.9	320	9	US-09-874-923-22	Sequence 22, Appl
79	15.9	320	10	US-09-874-923-55	Sequence 55, Appl
79	15.9	320	10	US-09-874-923-55	Sequence 121, App
79	15.9	709	9	US-09-991-496-121	Sequence 121, App
79	15.9	709	10	US-09-874-923-141	Sequence 44312, A
78	15.7	70	10	US-09-864-761-44312	Sequence 66, Appl
76	15.3	191	9	US-09-950-933A-66	Sequence 8, Appl
76	15.3	2441	12	US-10-109-886-8	

ALIGNMENTS

RESULT 1
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20030081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: 686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match	100.0%	Score 498;	DB 10;	Length 81;
Best Local Similarity	100.0%;	Pred. No. 1.5e-35;		
Matches	81;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYCCEYFDSLHACPCLRCSPTCOYCCF 60
Db 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYCCEYFDSLHACPCLRCSPTCOYCCF 60

QY 61 HSEYFDSLHACPPATCQPYC 81
Db 61 HSEYFDSLHACPPATCQPYC 81

RESULT 2
US-10-077-438-3
; Sequence 3, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:

```

; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match          46.3%; Score 230.5; DB 9; Length 207;
Best Local Similarity 57.8%; Pred. No. 5.7e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;
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QY 1 CSQNEFYDLSLHACIPCOLRCSSNTPLTCQRYCCCEYFDSLHAC-PC-LRCSPTQCYC 58
DB 46 CSQNEFYDLSLHACIPCOLRCSSNTPLTC-----LHACIPCOLRCSSNT----- 90
QY 59 CFHSEYFDSLHACPPATCQPYC 81
DB 91 -----PPLTCQRYC 99
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RESULT 3
US-10-077-137-3
; Sequence 3, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3
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Query Match 46.3%; Score 230.5; DB 9; Length 207;

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Best Local Similarity 57.8%; Pred. No. 5.7e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

QY 1 CSQNEFYDLSLHACIPCOLRCSSNTPLTCQRYCCCEYFDSLHAC-PC-LRCSPTQCYC 58
DB 46 CSQNEFYDLSLHACIPCOLRCSSNTPLTC-----LHACIPCOLRCSSNT----- 90
QY 59 CFHSEYFDSLHACPPATCQPYC 81
DB 91 -----PPLTCQRYC 99
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RESULT 4
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/Ap-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9
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Query Match 40.5%; Score 201.5; DB 10; Length 283;
Best Local Similarity 60.6%; Pred. No. 1.9e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;

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QY 1 CSQNEFYDLSLHACIPCOLRCSSNTPLTCQRYC-CEYFDSL-----LHACPC 47
DB 5 CSQNEFYDLSLHACIPCOLRCSSNTPLTCQRYCNASVTNAGGGGDKHTCP- 63
QY 48 LRCSPP 53
DB 64 -PCPAP 68
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RESULT 5
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/Ap-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7
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Query Match 40.4%; Score 201; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e-11;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 34
 DB 1 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 34

RESULT 6
 US-09-854-864-6
 ; Sequence 6, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; PRIOR FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 51
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-864-6

Query Match 40.4%; Score 201; DB 10; Length 51;
 Best Local Similarity 100.0%; Pred. No. 5.1e-11;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 34
 DB 5 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 38

RESULT 7
 US-09-854-864-21
 ; Sequence 21, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; PRIOR FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 21
 ; LENGTH: 58
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-864-21

Query Match 40.4%; Score 201; DB 10; Length 58;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 34
 DB 1 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 34

RESULT 8
 US-09-854-864-5
 ; Sequence 5, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; APPLICANT: YU, GANG
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; PRIOR FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 181
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-864-5

Query Match 40.4%; Score 201; DB 10; Length 181;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 34
 DB 5 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 38

RESULT 9
 US-10-077-438-1
 ; Sequence 1, Application US/10077438
 ; Patent No. US20020165156A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MacKay, Fabienne
 ; APPLICANT: Browning, Jeffrey
 ; APPLICANT: Ambrose, Christine
 ; APPLICANT: Tschoep, Jurg
 ; APPLICANT: Schneider, Pascal
 ; APPLICANT: Thompson, Jeffrey
 ; APPLICANT: Biogen, Inc.
 ; APPLICANT: Apotech R&D S.A.
 ; TITLE OF INVENTION: Baff Receptor (BCMA), An
 ; FILE REFERENCE: A080PCT
 ; CURRENT APPLICATION NUMBER: US/10/077,438
 ; CURRENT FILING DATE: 2002-02-18
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,378
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/181,684
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: homo sapien
 US-10-077-438-1

Query Match 40.4%; Score 201; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSNTTPTTCORYC 34

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Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 10
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurig
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 11
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurig
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 12
US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurig
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 13
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEIL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
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us-09-855-158-13.rapb

Tue Jan 7 10:36:46 2003

Query Match 27.3%; Score 136; DB 10; Length 185;
 Best Local Similarity 70.6%; Pred. No. 3.8e-05;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 QY 1 CSONEYPDSLHACIPCOLRCSNTPLTCORYC 34
 Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCOPYC 36
 Search completed: January 7, 2003, 09:54:54
 Job time : 6.09023 secs

TYPE: PRT
 ORGANISM: human-murine Consensus
 US-09-854-864-12
 Query Match 30.7%; Score 153; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 9.9e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 CEYFDSLHACPLRCSPTCOYC 58
 Db 4 CEYFDSLHACPLRCSPTCOYC 27

RESULT 14
 US-09-854-864-10
 ; Sequence 10, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; PRIOR FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-854-864-10

Query Match 28.0%; Score 139.5; DB 10; Length 281;
 Best Local Similarity 45.5%; Pred. No. 2.7e-05;
 Matches 30; Conservative 3; Mismatches 16; Indels 17; Gaps 3;
 QY 1 CSONEYPDSLHACIPCOLRCSNTPLTCORYCCEYFDSL--HACPC 47
 Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCOPYDPSVTSVKVGGGDKHTCP- 61
 QY 48 LRCSP 53
 Db 62 -PCPAP 66

RESULT 15
 US-09-854-864-11
 ; Sequence 11, Application US/09854864
 ; Patent No. US20020081296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THEILL, LARS EYDE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
 ; FILE REFERENCE: A-686B
 ; CURRENT APPLICATION NUMBER: US/09/854,864
 ; PRIOR FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: US 60/204,039
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/214,591
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-854-864-11

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:38:19 ; Search time 10.5564 Seconds
(without alignments)
543.836 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEYFDSLLHACIPCOLR.....SEYFDSLLHACPPATCPQYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	40.4	34	1 PCT-US02-34376-11	Sequence 11, Appl
2	201	40.4	34	6 US-10-281-053-11	Sequence 11, Appl
3	201	40.4	184	1 PCT-US02-34376-6	Sequence 6, Appl
4	201	40.4	184	1 PCT-US02-06001-39	Sequence 9, Appl
5	201	40.4	184	5 US-09-848-271-2	Sequence 2, Appl
6	201	40.4	184	6 US-10-281-053-6	Sequence 6, Appl
7	201	40.4	184	6 US-10-087-080-39	Sequence 39, Appl
8	100.5	20.2	334	6 US-10-258-368-8	Sequence 6, Appl
9	100.5	20.2	334	6 US-10-258-368-6	Sequence 6, Appl
10	93	18.7	166	6 US-10-293-816-6	Sequence 22, Appl
11	93	18.7	233	6 US-10-268-951-22	Sequence 1, Appl
12	93	18.7	233	6 US-10-258-368-1	Sequence 2, Appl
13	93	18.7	233	6 US-10-293-816-2	Sequence 12, Appl
14	93	18.7	301	6 US-10-258-368-12	Sequence 15, Appl
15	93	18.7	404	6 US-10-258-368-15	Sequence 15078, A
16	91.5	17.4	231	6 US-10-203-138A-15078	Sequence 2, Appl
17	86.5	16.8	1548	6 US-10-180-903-2	Sequence 2647, Ap
18	83.5	16.8	120	6 US-10-276-774-2647	Sequence 14491, A
19	83	16.7	93	6 US-09-724-676A-75263	Sequence 75263, A
20	81	16.3	1396	5 US-08-724-676A-75263	Sequence 75263, A
21	81	16.3	1396	5 US-08-724-676A-75263	Sequence 75262, A
22	81	16.3	1408	5 US-08-724-676A-75262	Sequence 75262, A
23	81	16.3	1408	5 US-08-724-676A-75262	Sequence 75261, A
24	81	16.3	1575	5 US-09-724-676A-75261	Sequence 75261, A
25	81	16.3	1575	5 US-09-724-676A-75261	Sequence 74753, A
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27	80.5	16.2	1167	5 US-09-724-676A-74762	Sequence 74762, A
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39	80.5	16.2	1609	5 US-09-724-676A-74757	Sequence 74757, A
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41	80.5	16.2	1610	5 US-09-724-676A-74757	Sequence 74757, A
42	80.5	16.2	1610	5 US-09-724-676A-74757	Sequence 74757, A
43	80.5	16.2	1610	5 US-09-724-676A-74757	Sequence 74757, A
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ALIGNMENTS

RESULT 1
PCT-US02-34376-11
Sequence 11, Application PC/TUS0234376
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Shu, Hong-Bing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Lianguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
FILE REFERENCE: 2879-86-PCT
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/345,106
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/348,962
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/354,966
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/403,364
PRIOR FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent in version 3.1
SEQ ID NO 11
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-34376-11
Query Match 40.4%; Score 201; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CSQNEYFDSLLHACIPCOLRCSNTPTLCQRYC 34
RESULT 2
US-10-281-053-11
Sequence 11, Application US/10281053
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Shu, Hong-Bing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Lianguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
FILE REFERENCE: 2879-86

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/ CURRENT APPLICATION NUMBER: US/10/281.053
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,106
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 60/348,962
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: 60/354,966
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/403,364
/ PRIOR FILING DATE: 2002-08-13
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 11
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-281-053-11

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Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 3
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/ Sequence 6, Application PC/TUS0234376
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
/ APPLICANT: Liu, Yingfang
/ APPLICANT: Xu, Liangguo
/ TITLE OF INVENTION: Three-Dimensional Structures of TRIL-1 and its Cognate Receptors
/ FILE REFERENCE: 2879-86-PCT
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,106
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 60/348,962
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: 60/354,966
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/403,364
/ PRIOR FILING DATE: 2002-08-13
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 6
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US02-34376-6

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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 4
PCT-US02-06001-39
/ Sequence 39, Application PC/TUS0206001
/ GENERAL INFORMATION:
/ APPLICANT: Mack, David H.
/ APPLICANT: Markowitz, Sanford David
/ APPLICANT: Eos Biotechnology, Inc.
/ APPLICANT: Case Western Reserve University
US-10-281-053-11

/ TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
/ TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
/ FILE REFERENCE: 018501-000840PC
/ CURRENT APPLICATION NUMBER: PCT/US02/06001
/ CURRENT FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: US 60/272,206
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: US 60/281,149
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: US 60/284,555
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 39
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
PCT-US02-06001-39

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Best Local Similarity 100.0%; Pred. No. 9.3e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 5
US-09-848-271-2
/ Sequence 2, Application US/09848271
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Ruben, Steven
/ TITLE OF INVENTION: Human Tumor Necrosis Factor TR18 and Methods Based Thereon
/ FILE REFERENCE: PFS26
/ CURRENT FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US/09/848,271
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/254,931
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/236,038
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: 60/201,852
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 2
/ LENGTH: 164
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-848-271-2

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Best Local Similarity 100.0%; Pred. No. 9.3e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41

RESULT 6
US-10-281-053-6
/ Sequence 6, Application US/10281053
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
/ APPLICANT: Liu, Yingfang
/ APPLICANT: Xu, Liangguo
US-10-281-053-6
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/ TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
/ FILE REFERENCE: 44158/254623
/ CURRENT APPLICATION NUMBER: US/10/293,816
/ CURRENT FILING DATE: 2002-11-12
/ PRIOR APPLICATION NUMBER: US 09/782,857
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: US 09/290,333
/ PRIOR FILING DATE: 1999-04-12
/ PRIOR APPLICATION NUMBER: US 08/810,572
/ PRIOR FILING DATE: 1997-03-03
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 166
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-816-6
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OY 52 -----PPTQYCC 59
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RESULT 11
US-10-268-951-22
/ Sequence 22 Application US/10268951
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Guo-Liang, et al.
/ TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
/ FILE REFERENCE: PF253P2
/ CURRENT APPLICATION NUMBER: US/10/268,951
/ PRIOR FILING DATE: 2002-10-11
/ PRIOR APPLICATION NUMBER: 10/082,260
/ PRIOR FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/879,919
/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 08/815,783
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: 60/328,401
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/293,812
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,978
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/254,875
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/241,952
/ PRIOR FILING DATE: 2000-10-22
/ PRIOR APPLICATION NUMBER: 60/211,537
/ PRIOR FILING DATE: 2000-06-15
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-268-951-22
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Best Local Similarity 28.4%; Pred. No. 0.1;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
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Db 91 SICGHPKQCAVFC 104
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RESULT 12
US-10-258-368-1
/ Sequence 1 Application US/10258368
/ GENERAL INFORMATION:
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Rennett, Paul
/ TITLE OF INVENTION: Taci As Anti-Tumor Agent
/ FILE REFERENCE: BIO0130 NP of PCT/US01/40626
/ CURRENT APPLICATION NUMBER: US/10/258,368
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US96/199,946
/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-258-368-1
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Best Local Similarity 28.4%; Pred. No. 0.1;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
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Db 91 SICGHPKQCAVFC 104
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RESULT 13
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/ Sequence 2 Application US/10293816
/ GENERAL INFORMATION:
/ APPLICANT: Bram, Richard J.
/ APPLICANT: Von Bulow, Gotz
/ TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
/ FILE REFERENCE: 44158/254623
/ CURRENT APPLICATION NUMBER: US/10/293,816
/ CURRENT FILING DATE: 2002-11-12
/ PRIOR APPLICATION NUMBER: US 09/782,857
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: US 09/290,333
/ PRIOR FILING DATE: 1999-04-12
/ PRIOR APPLICATION NUMBER: US 08/810,572
/ PRIOR FILING DATE: 1997-03-03
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-816-2
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Query Match 18.7%; Score 93; DB 6; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.1;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:39 ; Search time 59.4937 Seconds
(without alignments)
371.797 Million cell updates/sec

Title: US-09-855-158-15

Perfect score: 909

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	100.0	166	19 AAW75785	Human lymphocyte s
2	909	100.0	166	23 AAE15494	Human TACI extrace
3	909	100.0	265	22 AAE09244	Human TACI splice
4	909	100.0	293	19 AAW75783	Human lymphocyte s
5	909	100.0	293	21 AAB36312	Human neutrokin-a
6	909	100.0	293	21 AAY94000	A transmembrane ac
7	909	100.0	293	22 AAE09240	Human TACI protein
8	909	100.0	293	22 AAY71914	Human tumour necro
9	909	100.0	293	23 AAU99512	Human TACI-IgG Fc
10	909	100.0	293	23 ABB81488	Human TACI recepto

11	909	100.0	293	23 AAO14130	Human transmembran
12	909	100.0	293	23 AAW75408	Tumour necrosis fa
13	909	100.0	293	23 AAE15493	Human transmembran
14	909	100.0	293	23 AAU09900	Human AGP-3 relate
15	904	99.4	312	23 AAO14135	Protein of N-termi
16	904	99.4	397	23 AAE15498	Human TACI-immunog
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19	851	71.6	366	23 AAO14132	Protein of hTACI (
20	599	65.9	247	21 AAY93998	Human BR43x2, an i
21	490.5	54.0	334	23 AAO14133	Protein of hTACI (
22	419.5	46.1	249	21 AAY94006	A murine ztnf4, a
23	342	37.6	59	23 AAE15500	Human TACI cystein
24	279.5	30.7	57	23 AAU10953	Human AGP-3 recept
25	224	24.6	38	23 AAU10952	Human AGP-3 recept
26	218	24.0	37	23 AAU10951	Human TACI cystein
27	204	22.4	34	23 AAE15496	Human TACI cystein
28	201	22.1	33	23 AAE15495	Human AGP-3 recept
29	168	18.5	32	23 AAU10950	Human TANGO 140-2
30	95	10.5	197	21 AAB01421	Human polypeptide
31	93	10.2	1589	22 AAM42025	Human protein sequ
32	93	10.2	1727	22 AAB95554	Human polypeptide
33	93	10.2	1878	22 AAM40239	Human polypeptide
34	92	10.1	266	22 AAM39716	Human polypeptide
35	89	9.8	1878	19 AAW81170	Human BAZ2-alpha p
36	88.5	9.7	665	22 ABB68244	Drosophila melanog
37	88	9.7	795	22 ABG07025	Novel human diagno
38	87.5	9.6	463	20 AAV13392	Amino acid sequenc
39	87.5	9.6	463	21 AAB01373	Neuron-associated
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41	87.5	9.6	463	22 AAU12351	Human PRO328 polyp
42	87.5	9.6	463	22 AAB88408	Human membrane or
43	87.5	9.6	463	22 AAB60260	Human PRO328 prote
44	87.5	9.6	463	22 AAB53088	Human angiogenesis
45	87	9.6	251	22 AAE13153	Human mature stem

ALIGNMENTS

RESULT 1

AAW75785

ID AAW75785 standard; Protein; 166 AA.

AC AAW75785;

DT 18-JAN-1999 (first entry)

DE Human lymphocyte surface receptor extracellular domain.

KW TACI; transmembrane activator and CAML-interactor;

KW calcium signal-modulating cyclophilin ligand; human;

KW lymphocyte surface receptor; human; B-cell; B lymphocyte;

KW infection; cancer; rheumatoid arthritis; autoimmune disease;

KW glomerulonephritis; immunosuppressive; graft versus host disease;

KW transplant rejection; therapy; signal transduction.

OS Homo sapiens.

PN WO9839361-A1.

PD 11-SEP-1998.

PF 03-MAR-1998; 98WO-US04270.

PR 03-MAR-1997; 97US-0810572.

PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

PI Bram RJ, Von Bulow G;

DR WPI, 1998-506346/43.

DR N-PSDB; AAV57330.

XX New isolated transmembrane activator protein - used to develop
 PT products for treating e.g. infections, cancers, autoimmune and
 PT inflammatory conditions, transplant rejection or graft-versus-host
 PT disease
 PS Claim 8; Page 73; 89pp; English.
 XX This is the amino acid sequence of the N-terminal, i.e. the
 CC extracellular, domain of novel human transmembrane activator and
 CC CAML-interactor (TACI) protein (see AAW/5783). TACI is a lymphocyte
 CC receptor protein that is involved in the calcium activation pathway.
 CC It is normally present in B-lymphocytes, and to a much lesser extent
 CC in immature T-lymphocytes, and can therefore be targeted to
 CC specifically regulate B cell responses without affecting T cell
 CC activity. The extracellular domain of TACI functions as a binding
 CC site for a ligand that stimulates the activation of the cell by
 CC inducing the binding of the C-terminal portion (see AAW/5784) of
 CC TACI to the N-terminal domain of CAML. A recombinant form of the
 CC extracellular portion of TACI acts as a dominant-negative or
 CC blocking agent and acts to suppress the immune system. It can be
 CC used to treat or prevent autoimmune disease, graft rejection or
 CC graft versus host disease. The extracellular region is also used
 CC in a claimed method for identifying a ligand for TACI, in which
 CC binding of a candidate molecule is determined by detecting cellular
 CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT
 CC transcription factor, or of NF-AT dependent transcription.
 XX Sequence 166 AA;
 SQ
 Query Match 100.0%; Score 909; DB 19; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2,8e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
 DB 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
 QY 61 TCAAFCRSLSCRKEQGRFYDHLRLDCISGASICGQHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKEQGRFYDHLRLDCISGASICGQHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSDADQVALVYST 166
 DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSDADQVALVYST 166
 DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSDADQVALVYST 166
 RESULT 2
 ID AAE15494 standard; Protein; 166 AA.
 AC AAE15494;
 XX 12-MAR-2002 (first entry)
 DT Human TACI extracellular domain.
 DE Human TACI extracellular domain.
 XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX Homo sapiens.
 OS
 XX WO200187979-A2.
 XX 22-NOV-2001.
 PD 14-MAY-2001; 2001WO-US15567.
 PF

XX 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX (AMGE-) AMGEN INC.
 BA The111 LE, Yu G;
 XX WPI; 2002-066686/09.
 DR Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 XX Claim 1; Fig 12a; 94pp; English.
 PS The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus sequence of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung
 CC gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human TACI protein extracellular domain.
 XX Sequence 166 AA;
 SQ
 Query Match 100.0%; Score 909; DB 23; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2,8e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
 DB 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
 QY 61 TCAAFCRSLSCRKEQGRFYDHLRLDCISGASICGQHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKEQGRFYDHLRLDCISGASICGQHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSDADQVALVYST 166
 DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSDADQVALVYST 166
 DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSDADQVALVYST 166
 RESULT 3
 ID AAE09244 standard; Protein; 265 AA.
 AC AAE09244;
 XX 19-NOV-2001 (first entry)
 DT Human TACI splice variant protein.
 DE Human TACI splice variant protein.
 XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW psoriasis.
 XX Homo sapiens.
 OS

PN WO200160397-A1.
 XX 23-AUG-2001.
 PD 28-NOV-2000; 2000WO-US32378.
 PF 16-FEB-2000; 2000US-0182938.
 XX 22-AUG-2000; 2000US-0226986.
 PR (GETH) GENENTECH INC.
 XX PA Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 PI Yan M;
 XX WPI; 2001-541628/60.
 DR Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 XX activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists -
 XX Example 1; Fig 6; 160pp; English.
 PS The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 CC e.g. TACI or BCMA. The method is useful for treating pathological
 CC conditions or diseases associated with increased TALL-1 and APRIL
 CC expression or activity. TALL-1 and APRIL antagonists are used to
 CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
 CC They are useful for treating a mammal suffering from cancer such
 CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 CC psoriasis and lupus erythematosus. The present sequence is human
 CC TACI splice variant protein.
 XX Sequence 265 AA;
 SQ Query Match 100.0%; Score 909; DB 22; Length 265;
 Best Local Similarity 100.0%; Pred. No. 4.9e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MSGLGSRGRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLGTCTMCKTICNHQSOR 60
 DB 1 MSGLGSRGRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLGTCTMCKTICNHQSOR 60
 OY 61 TCAAFCSRSLSCRKEQKFDHLLRDCISCASTCGOHPKOCAYFCENKLRSPVNLPELRR 120
 DB 61 TCAAFCSRSLSCRKEQKFDHLLRDCISCASTCGOHPKOCAYFCENKLRSPVNLPELRR 120
 OY 121 QRSGEVNNDSNGRYQGLEHRGSEASPALGLKLSADQVALVYST 166
 DB 121 QRSGEVNNDSNGRYQGLEHRGSEASPALGLKLSADQVALVYST 166
 RESULT 4.
 AAW75783
 ID AAW75783 standard; Protein; 293 AA.
 XX AAW75783;
 AC 18-JAN-1999 (first entry)
 DT Human lymphocyte surface receptor TACI.
 DE TACI; transmembrane activator and CAML-interactor;
 XX calcium signal-modulating cyclophilin ligand; human;
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte;
 KW infection; cancer; rheumatoid arthritis; autoimmune disease;
 KW glomerulonephritis; immunosuppressive; graft versus host disease;
 KW transplant rejection; therapy.

OS Homo sapiens.
 XX Key Location/Qualifiers
 PH Domain 1..166
 FI /label= Extracellular_domain
 FI /note= "Claim 8"
 FI 167..186
 FI /label= Transmembrane_domain
 FI 187..294
 FI /label= Cytoplasmic_domain
 FT /note= "Claim 6"
 FT 34..71
 FT /note= "TNFR_NGFR motif"
 FT WO9839361-A1.
 XX 11-SEP-1998.
 PD 03-MAR-1998; 98WO-US04270.
 XX 03-MAR-1997; 97US-0810572.
 PR (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PA Bram RJ, Von Bulow G;
 PI WPI; 1998-506346/43.
 XX N-PSDB; AAV57328.
 DR New isolated transmembrane activator protein - used to develop
 PT products for treating e.g. infections, cancers, autoimmune and
 PT inflammatory conditions, transplant rejection or graft-versus-host
 PT disease
 XX Claim 20; Fig 2a; 89pp; English.
 PS This is the amino acid sequence of novel human transmembrane
 CC activator and CAML-interactor (TACI) protein, a lymphocyte receptor
 CC protein that is involved in the calcium activation pathway. TACI
 CC is normally present in B-lymphocytes, and to a much lesser extent
 CC in immature T-lymphocytes, and can therefore be targeted to cell
 CC specifically regulate B cell responses without affecting T cell
 CC activity. TACI cDNA (seeV57328) was isolated from a B-lymphocyte
 CC cDNA library using a yeast two-hybrid assay. Also claimed are
 CC the C-terminal (see AAW75784) and N-terminal (see AAW75785) fragments
 CC of TACI, recombinant DNA constructs, unicellular hosts, and
 CC antibodies to TACI protein. Methods are claimed for identifying a
 CC ligand for TACI and for identifying immunosuppressive drugs that
 CC selectively block the action of B lymphocytes without affecting
 CC mature T lymphocytes. TACI can be activated to increase immune
 CC system activity, e.g. for treating infections or cancers. It can
 CC be blocked to provide immunosuppression, e.g. for treating
 CC autoimmune and inflammatory conditions such as immune complex-
 CC induced vasculitis, glomerulonephritis, haemolytic anaemia,
 CC myasthenia gravis, type II collagen-induced arthritis, experimental
 CC allergic and hyperacute xenograft rejection, rheumatoid arthritis,
 CC systemic lupus erythematosus, transplant rejection, cancer or
 CC graft versus host disease.
 XX Sequence 293 AA;
 SQ Query Match 100.0%; Score 909; DB 19; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-93;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MSGLGSRGRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLGTCTMCKTICNHQSOR 60
 DB 1 MSGLGSRGRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLGTCTMCKTICNHQSOR 60
 OY 61 TCAAFCSRSLSCRKEQKFDHLLRDCISCASTCGOHPKOCAYFCENKLRSPVNLPELRR 120
 DB 61 TCAAFCSRSLSCRKEQKFDHLLRDCISCASTCGOHPKOCAYFCENKLRSPVNLPELRR 120

QY 121 ORSGEVNNSDNGRYOGLHHRGSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYOGLHHRGSEASPALPGLKLSADQVALVYST 166

RESULT 5
ID AAB36312 standard; Protein; 293 AA.
XX AAB36312:
XX AAB36312:
XX 26-FEB-2001 (first entry)

DE Human neutrokin- α binding protein TR17 SEQ ID NO:2.
XX Human neutrokin- α binding protein; NAR protein; TR17; cytostatic;
KW immunosuppressive; neutrotropic; neuroprotective; antiviral; antiallergic;
KW hepatotropic; antidiabetic; antinflammatory; antitumor; cardiant;
KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
KW autoimmune disorder.

OS Homo sapiens.
XX WO200058362-A1.
XX 05-OCT-2000.
XX 24-MAR-2000; 2000WO-US07966.
XX 26-MAR-1999; 99US-0126599.
XX 10-MAR-2000; 2000US-0188208.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Ullrich S, Baker K;
XX WPI: 2000-602359/57.
XX DR N-PSDB; AAC64602.

XX Nucleic acid encoding a neutrokin- α receptor (NAR) such as TR17,
PT useful for producing TR17 protein which is used in the treatment and
PT diagnosis of autoimmune and immunodeficiency disorders -
XX Claim 1; Fig 1; 398bp; English.

XX The present sequence represents the human neutrokin- α binding (NAR)
CC protein designated TR17. TR17 has cytostatic, immunosuppressive,
CC neutrotropic, neuroprotective, antiviral, antiallergic, hepatotropic,
CC antidiabetic, antinflammatory, antitumor, cardiant and ophthalmological
CC activities and can be used in gene therapy. The TR17 protein and
CC antibodies are useful for treating and diagnosing immunodeficiency
CC disorders and autoimmune disorders. The TR17 polypeptides,
CC polynucleotides, antibodies, agonists and/or antagonists are used for
CC treating various other diseases defined in the specification and as
CC research tools for studying the phenotypic effects that result from
CC inhibiting TR17/TR17 ligand interactions on various cell types.

XX Sequence 293 AA;

XX Query Match 100.0%; Score 909; DB 21; Length 293;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-83;
XX Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRSGRSRVDOERFPQGLMTGVAMRSCPEBOYWDPLGTGMSCKTICNHQSOR 60
Db 1 MSGLSRRSGRSRVDOERFPQGLMTGVAMRSCPEBOYWDPLGTGMSCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKEOGKFYDHLRLDQCISGQHFKQCAFCENKJRSFVNLPELRR 120
Db 61 TCAAFCRSLSCRKEOGKFYDHLRLDQCISGQHFKQCAFCENKJRSFVNLPELRR 120
QY 121 ORSGEVNNSDNGRYOGLHHRGSEASPALPGLKLSADQVALVYST 166

Db 121 ORSGEVNNSDNGRYOGLHHRGSEASPALPGLKLSADQVALVYST 166

RESULT 6
ID AAY94000 standard; Protein; 293 AA.
XX AAY94000:
XX AAY94000:
XX 20-OCT-2000 (first entry)

DE A transmembrane activator and CAML-interactor (TACI).
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumor necrosis factor; TNF;
KW TNF4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.

OS Homo sapiens.
XX WO200040716-A2.
XX 13-JUL-2000.
XX 07-JAN-2000; 2000WO-US00396.
XX 07-JAN-1999; 99US-0226533.
XX (ZYMO) ZYMOGENETICS INC.
XX Gross JA, Xu W, Madden K, Yee DP;
XX WPI: 2000-452538/39.
XX DR N-PSDB; AAA58558.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX Disclosure; Page 149-150; 175bp; English.

XX The present sequence represents a human transmembrane activator and
CC CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
CC or BCMA (a related B cell protein) receptor contain a cysteine rich
CC domain, and are used for inhibiting ztnf4 activity. Tnfr4 is a TNF
CC ligand. They are also used for inhibiting BR43x2, TACI or BCMA
CC receptor-ligand engagement associated with activated or resting B
CC lymphocytes effector T-cells or with antibody production. The
CC antibody production is associated with an autoimmune disease selected
CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
CC and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA
CC receptor-ligand engagement is associated with asthma, bronchitis,
CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
CC light chain neuropathy, amyloidosis, moderating immune response,
CC immunosuppression, graft rejection, graft versus host disease,
CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
CC polypeptides, fusions, antibodies, agonists or antagonists can be used
CC to treat hypertension, renal artery stenosis, or occlusion, and
CC cholesterol or renal emboli.

XX Sequence 293 AA;
XX Query Match 100.0%; Score 909; DB 21; Length 293;

Best Local Similarity 100.0%; Pred. No. 5.6e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGGRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
DB 1 MSGLGSRGGRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60

QY 61 TCAAFCSLSCKREQKFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPELRR 120
DB 61 TCAAFCSLSCKREQKFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPELRR 120

QY 121 QRSGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 7
AAE09240
ID AAE09240 standard; Protein; 293 AA.
XX
AC AAE09240;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human TACI protein.
XX
KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200160397-A1.
XX
PD 23-AUG-2001.
XX
PF 26-NOV-2000; 2000WO-US32378.
XX
PR 16-FEB-2000; 2000US-0182938.
PR 22-AUG-2000; 2000US-0226986.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan M;
XX
DR N-PSDB; AAD15901.
XX
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
PS Example 1; Fig 1; 160pp; English.
XX
CC The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
CC TACI protein.
XX
SQ Sequence 293 AA;
Query Match 100.0%; Score 909; DB 22; Length 293;

Best Local Similarity 100.0%; Pred. No. 5.6e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGGRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
DB 1 MSGLGSRGGRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60

QY 61 TCAAFCSLSCKREQKFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPELRR 120
DB 61 TCAAFCSLSCKREQKFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPELRR 120

QY 121 QRSGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 8
AAAY71914
ID AAY71914 standard; Protein; 293 AA.
XX
AC AAY71914;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor (TACI) protein.
XX
KW Human; transmembrane activator and CAML interactor; TACI;
KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
KW neutrophilic alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;
KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;
KW antiarthritic; antineumatic; immunosuppressive; multiple sclerosis;
KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
KW cell death; immunoglobulin E-mediated allergic reaction; IGE.
XX
OS Homo sapiens.
XX
FH Key
FT Domain
FT 2..166
FT /label= Extracellular domain
FT /notes= "Binds with amino acids 123-285 of extracellular
FT domain of TACI-L"
XX
PN WO200067034-A1.
XX
PD 09-NOV-2000.
XX
PF 14-APR-2000; 2000WO-US10282.
XX
PR 30-APR-1999; 99US-0302863.
XX
PA (IMMU) IMMUNEX CORP.
XX
PI Goodwin RG, Din WS;
XX
DR WPI; 2001-016005/02.
DR N-PSDB; AAD02006.
XX
PT Use of new interactions between tumour necrosis factor receptors (TACI)
PT and TACI ligands to screen candidate molecules for determining agonist
PT and antagonist interactions which are used for treating inflammation -
XX
PS Claim 10; Fig 1b; 46pp; English.
XX
CC The present sequence is a human tumour necrosis factor receptor (TACI)
CC protein. TACI (Transmembrane activator and calcium-signal modulating
CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin
CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of
CC TACI/TACI-L complex is useful for modulating an intracellular signalling
CC cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L
CC complex are used to inhibit the interaction between TACI and TACI-L for
CC therapeutic purposes to treat tumour and tumour metastasis and to combat
CC various autoimmune diseases e.g. multiple sclerosis and diabetes, as

CC well as other disorders, such as viral infection, rheumatoid arthritis,
CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
CC and inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L
CC acts upon.

CC Sequence 293 AA;

Query Match 100.0%; Score 909; DB 22; Length 293;

Best Local Similarity 100.0%; Pred. No. 5.6e-83;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRRGRRVDOERFPQGLMTGVAMRSCPEBQIWDPLIGTCMCKTICNHQSOR 60
DB 1 MSGIGSRGRRGRRVDOERFPQGLMTGVAMRSCPEBQIWDPLIGTCMCKTICNHQSOR 60
QY 61 TCAAFCRSLSCREKQGFYDHLRDCISCSICQHPKQCAFCEKRLRSVNLPEELRR 120
DB 61 TCAAFCRSLSCREKQGFYDHLRDCISCSICQHPKQCAFCEKRLRSVNLPEELRR 120
QY 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 9

AAU99512 standard; Protein; 293 AA.

AAU99512;

07-OCT-2002 (first entry)

Human TACI-IgG Fc fusion protein.

Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
immunoglobulin production; B-cell proliferation; immune system disorder;
autoimmune disease; cancer; lymphoproliferative disorder; pain;
microbial infection; parasitic infection; bone disease; atherosclerosis;
cardiovascular disorder; neurodegenerative disease; wound healing;
graft versus host disease; haematopoietic cell disorder; nephritis;
transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG;
immunoglobulin G; Fc portion.

Homo sapiens.

US2002064829-A1.

30-MAY-2002.

14-JUN-2001; 2001US-0879919.

14-MAR-1996; 96US-016812P.
15-JUN-2000; 2000US-211537P.
23-OCT-2000; 2000US-241952P.
13-DEC-2000; 2000US-254875P.
16-MAR-2001; 2001US-276248P.
23-MAR-2001; 2001US-277978P.
25-MAY-2001; 2001US-293499P.
12-MAR-1997; 97US-0815783.

(HUMA-) HUMAN GENOME SCI INC.

Yu G, Ni J, Gentz RL, Dillon PJ;

WPI; 2002-556722/59.

Novel human multimeric tumour necrosis factor delta or epsilon protein
useful for treating disease or disorder of immune system such as
autoimmune disease, immunodeficiency, or cancer of immune system

XX Example 29; Page 125; 143pp; English.

XX The present invention relates to the isolation of human tumour necrosis
XX factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
XX sequences encoding them. The proteins are useful for modulating
XX immunoglobulin production or for modulating proliferation of B-cells.
XX The sequences of the invention are useful for treating diseases or
XX disorders of the immune system. Such disorders include autoimmune
XX diseases (e.g. systemic lupus erythematosus (SLE), acquired
XX immunodeficiency syndrome (AIDS)), cancers of the immune system
XX (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
XX non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
XX disorders, microbial infections (e.g. viral, bacterial), parasitic
XX infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
XX pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
XX neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
XX disease), graft versus host disease, wound healing, haematopoietic cell
XX disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
XX diseases or disorders associated with various mucous membranes of the
XX body (e.g. mucositis), and disorders of the pulmonary system. The
XX proteins are also useful as a vaccine adjuvant that enhances immune
XX responses to specific antigens. The present sequence for human
XX transmembrane activator and CAML-interactor (TACI)-immunoglobulin G
XX (IgG) Fc fusion protein is used in the examples of the present
XX invention.

Sequence 293 AA;

Query Match 100.0%; Score 909; DB 23; Length 293;

Best Local Similarity 100.0%; Pred. No. 5.6e-83;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRRGRRVDOERFPQGLMTGVAMRSCPEBQIWDPLIGTCMCKTICNHQSOR 60
DB 1 MSGIGSRGRRGRRVDOERFPQGLMTGVAMRSCPEBQIWDPLIGTCMCKTICNHQSOR 60
QY 61 TCAAFCRSLSCREKQGFYDHLRDCISCSICQHPKQCAFCEKRLRSVNLPEELRR 120
DB 61 TCAAFCRSLSCREKQGFYDHLRDCISCSICQHPKQCAFCEKRLRSVNLPEELRR 120
QY 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 10

ABB81488 standard; Protein; 293 AA.

ABB81488;

02-SEP-2002 (first entry)

Human TACI receptor related protein SEQ ID NO:8.

Human; Znf112; tumour necrosis factor receptor; cytosolic;
immunosuppressive; dermatological; antiinflammatory; antidiabetic;
neuroprotective; antirheumatic; antitachycardic; antiaesthetic;
neurotropic; hypotensive; gene therapy; B lymphocyte; tumour;
autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
multiple sclerosis; insulin dependent diabetes mellitus; asthma;
rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
myelomaphthis; renal neoplasia; multiple myeloma; amyloidosis;
light chain neuropathy; hypertension; large vessel disease;
graft-versus host disease; graft rejection; Crohn's disease.

Homo sapiens.

WO200238766-A2.

16-MAY-2002.

XX	05-NOV-2001; 2001WO-US47018.
PP	
FF	
XX	
PR	07-NOV-2000; 2000US-246449P.
PR	20-DEC-2000; 2000US-257131P.
PR	28-AUG-2001; 2001US-301715P.
PR	29-JUN-2001; 2001US-315565P.
XX	(ZYMO) ZYMOGENETICS INC.
PA	
XX	
XX	Gross JA, Xu W, Henne RM, Grant FJ;
PI	WPI; 2002-508212/54.
DR	
XX	
PT	Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT	Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
PT	stage renal failure or renal disease and lymphoma -
PT	
XX	Disclosure; Page 136-137; 154pp; English.
XX	
CC	The present invention describes a human tumour necrosis factor receptor
CC	designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC	dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC	antirheumatic, antiarthritic, anaesthetic, nephrotropic and hypotensive
CC	activities, and can be used in gene therapy. (I) can be used for
CC	inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC	(e.g. ZTNF4), for treating disorders and diseases associated with B
CC	lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC	inhibiting the proliferation of tumour cells (I) is useful for treating
CC	autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC	gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC	rheumatoid arthritis, bronchitis, insulin dependent diabetes mellitus, asthma,
CC	or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC	leukaemia, nephritis, and pyelonephritis, and for treating renal
CC	neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC	amyloidosis, hypertension, large vessel diseases, graft-versus host
CC	disease, graft rejection and Crohn's disease. (I) is useful for
CC	modulating the immune system, for regulating B cell responses and
CC	development, for modulating development of other cells, antibody
CC	production and cytokine production, and for modulating T and B cell
CC	communication. The present sequence represents a protein which is
CC	given in the exemplification of the present invention.
XX	
XX	Sequence 293 AA;
XX	
Query Match	100.0%; Score 909; DB 23; Length 293;
Best Local Similarity	100.0%; Pred. No. 5.6e-83;
Matches 166; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MSGLGRSGRGSRVDQERFPQGLWTGVAMRSPCEEQYWDPLLGTCMSCKTICNHQSQR 60
Db	1 MSGLGRSGRGSRVDQERFPQGLWTGVAMRSPCEEQYWDPLLGTCMSCKTICNHQSQR 60
Qy	61 TCAAFCRSLSCRKEQGKFDYHLLRDICISCASTCGOHPKQCAFCEKNLRSPVNLPPELR 120
Db	61 TCAAFCRSLSCRKEQGKFDYHLLRDICISCASTCGOHPKQCAFCEKNLRSPVNLPPELR 120
Qy	121 ORSGEVNNDNSGRVQGLEHRGSSASPALPCLKLSDOVALVYST 166
Db	121 ORSGEVNNDNSGRVQGLEHRGSSASPALPCLKLSDOVALVYST 166
RESULT 11	
AAOI4130	
ID	AAOI4130 standard; Protein; 293 AA.
AC	XX
AC	AAOI4130;
XX	
DT	02-MAY-2002 (first entry)
XX	
DE	Human transmembrane activator CAML interactor protein (TACI).
XX	
KW	Human transmembrane activator CAML interactor protein; TACI cytosolic;

KW	cell proliferation; tumour; vulnery;	renal cell cancer; mastocytoma;
KW	Kaposi's sarcoma; breast; ovarian carcinoma;	rectal; throat; melanoma;
KW	colon; bladder; mammary adenocarcinoma;	gastrointestinal; hyperplasia;
KW	pharyngeal squamous cell; stomach;	cellular hyperproliferation; pannus;
KW	scleroderma; rheumatoid arthritis;	scarring; liver; lung fibrosis;
XX	uterine.	
OS	Homo sapiens.	
OS		
FH	Key	Location/Qualifiers
FT	Domain	1..114
XX		/label= Extracellular_domain
XX	WO200181417-A2.	
PN		
XX		
PD	01-NOV-2001.	
XX		
PF	27-APR-2001; 2001WO-US40626.	
XX		
PR	27-APR-2000; 2000US-199946P.	
PA	(BIOJ) BIOGEN INC.	
PA	(APOT-) APOTECH R & D SA.	
XX		
PI	Ambrose C, Thompson J, Schneider P, Rennett P;	
DR	WPI: 2002-062027/08.	
DR	N-PSDB; AAK98726.	
XX		
PT	Treating mammal for condition associated with undesired cell	
PT	proliferation e.g.; solid tumour or reducing solid tumour size located in	
PT	mammal comprises administering transmembrane activator CAML interactor	
PT	protein reagent -	
XX	Claim 8; Fig 1; 42pp; English.	
XX		
CC	This sequence represents the human transmembrane activator CAML	
CC	interactor protein (TACI). The invention relates to treating a mammal for	
CC	a condition associated with undesired cell proliferation (e.g. a solid	
CC	tumour, or reducing the size of a solid tumour located on or in a mammal)	
CC	comprising administering a transmembrane activator CAML interactor	
CC	protein (TACI) reagent. The TACI reagent has cytostatic and vulnery	
CC	activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or	
CC	cat) for a condition associated with undesired cell proliferation (e.g.	
CC	cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,	
CC	sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon	
CC	cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,	
CC	pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach	
CC	cancer).	
CC	The method is also useful for treating cellular	
CC	hyperproliferation (hyperplasia) such as scleroderma, pannus formation in	
CC	rheumatoid arthritis, post-surgical scarring and lung, liver and uterine	
CC	fibrosis. The TACI reagent of the invention can extend mean survival time	
CC	of a mammal by 25% as compared to the mean survival time of a mammal in	
CC	the absence of administering the TACI reagent. The TACI reagent also	
CC	reduces the size of the tumour by 25% or more.	
XX		
SQ	Sequence 293 AA;	
	Query Match 100.0%; Score 909; DB 23; Length 293;	
	Best Local Similarity 100.0%; Pred. NO.5.6e-83;	
	Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 MSGLGRRRGGRGSRVDDEERFPQGLWTGVAMRSCFERQYWDPLGTGCMCKTCNHQSQR 60	
Db	1 MSGLGRRRGGRGSRVDDEERFPQGLWTGVAMRSCFERQYWDPLGTGCMCKTCNHQSQR 60	
OY	61 TCAAFCRSLSCRKEQGKFYDHLRLDCISCSASICQHPKQCAFCENKLRSVPNLPPELR 120	
Db	61 TCAAFCRSLSCRKEQGKFYDHLRLDCISCSASICQHPKQCAFCENKLRSVPNLPPELR 120	
OY	121 QRSGEVNNDNGRYOGLHRGSEASPALFGLKLSADQVALVYST 166	
Db	121 QRSGEVNNDNGRYOGLHRGSEASPALFGLKLSADQVALVYST 166	

RESULT 12
 AAU75408
 ID AAU75408 standard; Protein; 293 AA.
 XX
 AC AAU75408;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Tumour necrosis factor (TNF) receptor TACI-FC fusion.
 XX
 KW Tumour necrosis factor; TNF; cytostatic; arteriosclerosis;
 KW analgesic; cerebroprotective; neurotropic; neuroprotective; hepatotropic;
 KW immunoglobulin production; B cell proliferation; immunosuppressive;
 KW HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
 KW Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
 KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
 KW acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
 KW chronic lymphocytic leukaemia; lymphoproliferative disorder;
 KW bacterial infection; viral infection; osteoporosis; atherosclerosis;
 KW pain; cardiovascular disease; stroke; allergy; Alzheimer's disease;
 KW neurodegenerative disease; inflammation; liver disease; cirrhosis;
 KW cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
 KW ulcerative colitis; angiogenesis; septic shock; wound healing;
 KW tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200196528-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US19026.
 XX
 PR 15-JUN-2000; 2000US-211537P.
 PR 13-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Yu G, Ni J, Gentz RL, Dillon RJ, Hilbert D;
 XX
 DR WPI; 2002-130727/17.
 DR N-PSDB; ABK13415.
 XX
 XX Novel multimeric human tumour necrosis factor delta or epsilon protein
 PT useful for treating cancer, immune system disorders, infection,
 PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
 PT psoriasis -
 XX
 PS Example 29; Page 341-342; 344pp; English.
 XX
 CC The invention describes a multimeric human tumour necrosis factor (TNF)
 CC delta or epsilon protein (I). (I) or a composition containing them (II)
 CC are useful for modulating immunoglobulin production or proliferation of B
 CC cells. (II) or (I) is useful for treating a disease or disorder of the
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
 CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
 CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
 CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis, for promoting
 CC angiogenesis and wound healing, as a diagnostic research reagent, as an

CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
 CC receptor; in apoptosis of transformed cell lines; mediation of cell
 CC activation and proliferation; and as an immunogen to produce (II). (II)
 CC is useful to purify, detect and target (I), for measuring levels of (I)
 CC in biological samples, for immunophenotyping samples, and to treat,
 CC inhibit or prevent diseases and disorders associated with aberrant
 CC expression and/or activity of (I). This is the amino acid sequence of a
 CC fusion protein of tumour necrosis factor receptor TACI and immunoglobulin
 CC G (IgG) crystallisation fragment, described in the method of the
 CC invention.
 XX
 SQ Sequence 293 AA;
 XX
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5, 6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGLSRSGRGRSRVDOEERPPQGLMTGVAMRSCPEBYMDPLGTGMSCKTICNHSOR 60
 DB 1 MSGLSRSGRGRSRVDOEERPPQGLMTGVAMRSCPEBYMDPLGTGMSCKTICNHSOR 60
 QY 61 TCAATCRSLSCREKGGKTYDHLRDCISCASICGHPKQCAIFCENKLRSPVNLPEELRR 120
 DB 61 TCAATCRSLSCREKGGKTYDHLRDCISCASICGHPKQCAIFCENKLRSPVNLPEELRR 120
 QY 121 ORSGEVNNSDNGSRVQGLERHGSFASPALPOLKLSADQVALVYST 166
 DB 121 ORSGEVNNSDNGSRVQGLERHGSFASPALPOLKLSADQVALVYST 166
 XX
 RESULT 13
 AAEL15493
 ID AAEL15493 standard; Protein; 293 AA.
 XX
 AC AAEL15493;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human transmembrane activator and intracellular CAML interactor protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Region 34..66 /note= "Cysteine-rich consensus region"
 FT Region 71..104 /note= "Cysteine-rich consensus region"
 FT Domain 167..186 /label= Transmembrane_domain
 XX
 MO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;

DR WPI; 2002-066686/09.
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX Disclosure; Fig 12A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX is human TACI protein.
XX
XX Sequence 293 AA;
XX
XX Query Match 100.0%; Score 909; DB 23; Length 293;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-83;
XX Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSGLGRSRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMCKTICNHQSQR 60
XX DB 1 MSGLGRSRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMCKTICNHQSQR 60
XX QY 61 TCAAFCSLSCKRQKGFYDHLRDCISCAICGQHPKQCAFCENKLRSPVNLPELRR 120
XX DB 61 TCAAFCSLSCKRQKGFYDHLRDCISCAICGQHPKQCAFCENKLRSPVNLPELRR 120
XX QY 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
XX DB 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
XX
XX RESULT 14
XX AAU09900
XX ID AAU09900 standard; Protein; 293 AA.
XX AC AAU09900;
XX XX
XX 12-MAR-2002 (first entry)
XX
XX Human AGP-3 related protein receptor.
XX
XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
KW multiple sclerosis; Parkinson's disease; transgenic animal.
XX
XX Homo sapiens.
XX OS
XX XX
XX PN
XX ID WO200185782-A2.
XX XX

PD 15-NOV-2001.
XX
XX 12-FEB-2001; 2001WO-US04568.
XX
XX 11-FEB-2000; 2000US-181800P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Boyle WJ, Hsu H;
XX
XX WPI; 2002-049441/06.
XX N-PSDB; AAS18558.
XX
XX Composition, useful for identifying modulator of receptor for treating
PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
PT ligand family member) receptor and encoding nucleic acids -
XX
XX Disclosure; Page 117-119; 124pp; English.
XX
XX The invention relates to a composition (I) comprising AGP-3 receptor
CC (tumour necrosis factor ligand family member) related protein (II)
CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
CC assays to identify cells and tissues that express AGP-3R or proteins
CC related to AGP-3R-related protein and for identifying compounds
CC (agonists or antagonists) that interact with AGP-3R proteins. (II) is
CC also useful for identifying intracellular proteins that interact with
CC the respective cytoplasmic domains by yeast two-hybrid screening
CC process. (II) is involved in B cell growth, survival and activation
CC particularly in lymph node, spleen, and Peyer's patches. AGP-3R
CC agonists and antagonists identified using (II) are used for modulating
CC B cell response and are used to treat diseases characterised by
CC inflammatory processes or deregulated immune response such as
CC rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
CC lupus, etc. (II) is also useful in the production of hybridoma cells
CC which are derived from B cells which involve treating the hybridoma
CC cells with (II). (II) is useful in the treatment of inflammatory
CC conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
CC (II), its agonists or antagonists are useful for treating acute
CC pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
CC asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
CC glomerulonephritis, inflammatory bowel disease, ischaemic injury
CC including cerebral ischaemia, multiple myeloma, multiple sclerosis,
CC osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
CC shock, etc. The nucleic acids are also useful for developing transgenic
CC animals expressing (II), which are useful for producing the polypeptides
CC and for the study of in vivo biological activity. The present sequence
CC represents the amino acid sequence of human AGP-3 related protein
XX receptor.
XX
XX Sequence 293 AA;
XX
XX Query Match 100.0%; Score 909; DB 23; Length 293;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-83;
XX Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSGLGRSRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMCKTICNHQSQR 60
XX DB 1 MSGLGRSRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMCKTICNHQSQR 60
XX QY 61 TCAAFCSLSCKRQKGFYDHLRDCISCAICGQHPKQCAFCENKLRSPVNLPELRR 120
XX DB 61 TCAAFCSLSCKRQKGFYDHLRDCISCAICGQHPKQCAFCENKLRSPVNLPELRR 120
XX QY 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
XX DB 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
XX
XX RESULT 15
XX AA014135
XX ID AA014135 standard; Protein; 312 AA.
XX XX

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 23.7143 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-15
Perfect score: 909
Sequence: 1 MSGLGRSRGRSRVDQER.....SPALPGLKLSADQVALVYST 166
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.5	10.7	1548	2 S34583	serine proteinase
2	86.5	9.5	353	2 T06466	cathepsin B-like c
3	86	9.5	1299	2 T43251	furin (EC 3.4.21.7
4	84.5	9.3	355	2 AD0299	conserved hypothet
5	83	9.1	13288	2 T03099	mucin, submaxillar
6	82.5	9.1	899	2 G02428	subtilisin-like pr
7	82.5	9.1	915	2 J06148	subtilisin-like pr
8	82	9.0	932	2 I52527	PACE4A - mouse lfr
9	82	9.0	1650	2 S63457	dominant autoantig
10	82	9.0	4660	2 T42737	gp330 protein prec
11	81	8.9	773	1 JH0609	protein-tyrosine-p
12	81	8.9	1124	1 I5382	gene PACE4 protein
13	80.5	8.9	937	2 I5388	hypothetical prote
14	80	8.8	108	2 H9834	hypothetical prote
15	80	8.8	330	2 T25169	hypothetical prote
16	80	8.8	996	2 J0237	apolipoprotein E r
17	79.5	8.7	1984	2 T13171	probable vitelloge
18	79	8.7	269	2 C69312	molybdopterin oxid
19	78.5	8.6	630	2 A49656	estrogen-responsiv
20	78.5	8.6	1170	2 A53612	laminin B1k chain
21	78	8.6	596	2 A45664	variant-specific s
22	77.5	8.5	230	2 T19364	hypothetical prote
23	77.5	8.5	2195	2 T34264	hypothetical prote
24	77.5	8.5	2871	2 AF5624	fibritin-1 precu
25	77	8.5	620	2 AF0273	probable iron-sulf
26	77	8.5	751	2 T15230	hypothetical prote
27	77	8.5	1184	2 T09484	cartilage intermed
28	76.5	8.4	1680	2 A43434	furin (EC 3.4.21.7
29	76.5	8.4	1872	2 J04976	plexin 3 precursor

30	76	8.4	367	2 T45812	dnaJ-like protein
31	76	8.4	574	2 B88465	protein B0244.8 [i
32	76	8.4	915	2 B48225	probable proprotei
33	76	8.4	1748	2 S42136	cnjB protein - Tet
34	75.5	8.3	427	2 S38032	hypothetical prote
35	75.5	8.3	1620	2 T27283	subtilisin-like pr
36	75	8.3	962	2 J05571	subtilisin-like pr
37	75	8.3	965	1 A39490	subtilisin-like pr
38	75	8.3	975	2 T05870	subtilisin-like pr
39	75	8.3	2664	2 T28626	variant-specific s
40	75	8.3	3002	2 A47221	fibritin 1 precu
41	75	8.3	4544	1 S02392	alpha-2-macroglobu
42	75	8.3	4545	1 S25111	alpha-2-macroglobu
43	74.5	8.2	382	1 S48748	protein-tyrosine-p
44	74.5	8.2	501	2 I61512	TNF receptor assoc
45	74.5	8.2	773	2 I46059	beta-1 integrin su

ALIGNMENTS

RESULT 1
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:DL7583; NID:G407344; PIDN:BAA04507.1; PID:dl005033; PID:G440374
C:Keywords: hydrolase; serine proteinase

Query Match 10.7%; Score 97.5; DB 2; Length 1548;
Best Local Similarity 30.2%; Pred. No. 1;
Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

QY 14 RVDDQ--ERRFPQGLWTGVAMRSCEEQYWDPLLG--TCMSCKTICN-----HQSORITCAAF 65
DB 627 RADKHGQERF---LYHGECLENCVPVGHY--PAKGHTCLPCPDNCELVCYNPHICRCMSGY 681

QY 66 -----CRSLSCRKEQKQKPYDHLRLDCISCASIC 93
DB 682 VIIPNHTCQKLECR--QGEFQDSEYECEMPCERGC 715

RESULT 2

T06466
cathepsin B-like cysteine proteinase (EC 3.4.22.-) (Clone A116) - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T06466
R:Cejudo, F. J.; Murphy, G.; Chinoy, C.; Baulcombe, D. C.
Plant J. 2, 937-948, 1992
A:Title: A gibberellin-regulated gene from wheat with sequence homology to cathepsin B
A:Reference number: Z15659; MUID:93259430; PMID:1302642
A:Accession: T06466
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <CEJ>
A:Cross-references: EMBL:X66013; NID:g21698; PIDN:CAA46811.1; PID:g21699
A:Experimental source: cv. Chinese Spring, etiolated shoots
C:Genetics:
A:Note: Introns positions not resolved (incomplete sequence)
C:Superfamily: papain
C:Keywords: cysteine proteinase; glycoprotein; hydrolase

Query Match 9.5%; Score 86.5; DB 2; Length 353;

QY 100 CAYFCENKLR-SPVNL 114
Db 13192 CCYCKSSCKPSPVNV 13207

RESULT 6

G02428
subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
C:Accession: G02428
R:Reudelhuber, T.L. L
submitted to the EMBL Data Library, February 1996
A:Reference number: H01242
A:Accession: G02428
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-899 <REU>
A:Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C:Genetics:
A:Gene: PCS
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:148-386/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 899;
Best Local Similarity 26.0%; Pred. NO. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEQYWDPLLTGCMSCKTIQNHQSORTCAAF-----SLSC 71
Db 703 TNSCVTHCPDGSYQDTKNLCKKSENC-----KICTEFHNCTECRDGLSLQSGRCVSC 757
QY 72 RKEQGFYDHLRLDCISCASC-----GOHPKQC-----AYFCEN 106
Db 758 --EDGRYFNG--QDCQPCHRFCATCAGAGDGCINCTEGYFME 797

RESULT 7

JC6148
subtilisin-like proprotein convertase (EC 3.4.21.-) homolog - human
N:Alternate names: pCaA protease
C:Species: Homo sapiens (man)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: JC6148
R:Miranda, L.; Wolf, J.; Pichuanes, S.; Duke, R.; Franzusoff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A:Title: Isolation of the human pCa gene encoding the putative host protease for HIV-1
A:Reference number: JC6148; MUID:96353880; PMID:8755538
A:Contents: CEM T-cell
A:Accession: JC6148
A:Molecule type: mRNA
A:Residues: 1-915 <MR>
A:Cross-references: GB:U56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C:Comments: This protein functions as a soluble enzyme within the secretory pathway. It
C:Genetics:
A:Gene: pCaA
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:164-402/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. NO. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEQYWDPLLTGCMSCKTIQNHQSORTCAAF-----SLSC 71
Db 719 TNSCVTHCPDGSYQDTKNLCKKSENC-----KICTEFHNCTECRDGLSLQSGRCVSC 773
QY 72 RKEQGFYDHLRLDCISCASC-----GOHPKQC-----AYFCEN 106
Db 774 --EDGRYFNG--QDCQPCHRFCATCAGAGDGCINCTEGYFME 813

RESULT 8

I52527
PACE4A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I52527
R:Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A:Title: PACE4A is a ubiquitous endoprotease that has similar but not identical substrate
A:Reference number: I52527
A:Accession: I52527
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-932 <RES>
A:Cross-references: GB:D50060; NID:g769700; PIDN:BA08777.1; PID:g769701
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F:172-410/Domain: subtilisin homology <SBT>

Query Match 9.0%; Score 82; DB 2; Length 932;
Best Local Similarity 25.0%; Pred. NO. 16;
Matches 28; Conservative 16; Mismatches 44; Indels 24; Gaps 5;
QY 16 DOERFPQGLWTGVAMRSCPEEQYWDPLLTGCMSCK--TICNHQSORTCAAFCSLSCK 73
Db 650 DEEE-----YGVCHPECGDKGCGDNADCLNCVHFLSGNSKTNKVCVSEC----- 696
QY 74 EQGKFYDHLRLDCISCASC-----GOHPKQC-----AYFCENKLRSPVNLPP 116
Db 697 PLGVFGDAARCRCHKGCETCTGRSPAQLSCRCRGFYHHQETNTCVTLCP 748

RESULT 9

S53457
dominant autoantigen gp 330 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
C:Accession: S53457
R:Jokhadze, G.G.; Oleinikov, A.V.; Kanalas, J.J.; Makker, S.P.
Biochem. J. 305, 711-713, 1995
A:Title: Different molecular forms of rat kidney gp330, the dominant autoantigen of acti
A:Reference number: S53457; MUID:95151000; PMID:7848267
A:Accession: S53457
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1650 <JOK>
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F:29-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:72-106/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:111-147/Domain: EGF homology <EG1>
F:153-188/Domain: EGF homology <EG2>
F:196-235/Domain: LDL receptor WYTD-containing repeat homology <YW01>
F:236-278/Domain: LDL receptor WYTD-containing repeat homology <YW03>
F:279-329/Domain: LDL receptor WYTD-containing repeat homology <YW04>
F:330-373/Domain: LDL receptor WYTD-containing repeat homology <YW05>
F:374-414/Domain: LDL receptor WYTD-containing repeat homology <YW06>
F:415-457/Domain: LDL receptor WYTD-containing repeat homology <YW06>
F:466-505/Domain: EGF homology <EG3>
F:509-545/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:550-586/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:595-631/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:636-672/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:679-715/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:720-755/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:760-794/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:799-833/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:843-879/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:884-921/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:929-963/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:971-1006/Domain: EGF homology <EG4>
F:1012-1048/Domain: EGF homology <EG5>
F:1055-1099/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW07>

F/1100-1154/Domain: LDL receptor WTD-containing repeat homology #status atypical <YW08>
F/1155-1188/Domain: LDL receptor WTD-containing repeat homology #status atypical <YW08>
F/1189-1233/Domain: LDL receptor WTD-containing repeat homology <YW10>
F/1234-1273/Domain: LDL receptor WTD-containing repeat homology <YW11>
F/1274-1316/Domain: LDL receptor WTD-containing repeat homology <YW12>
F/1326-1359/Domain: EGF homology <EG6>

Query Match 9.0%; Score 82; DB 2; Length 1650;
Best Local Similarity 25.8%; Pred. No. 26;
Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

33 SCPEBOY-WDPULGTGCMCKTICNHQ---SQTCAAFGRSLSCRKEGKPYDH----- 81
Db 71 TCFPHQFPCDN--GHCIEKGRVCHNHVDDCSNDSDEKGGICNECLDSSISRCDHCTDTIT 128
Qy 82 -----LNRDCTICASI--CGQHPKOCATPCENKLRSPV-NLPPELRQRSGEVE 127
Db 129 SFYSCGLPGYKLMDSKRCVDIDECKESPQLCSQKCEVNVGSYICKCAPGYIREPDGKSC 188
Qy 128 NNSDN-----SGRY--QGLEHRSSEASPALPGL 153
Db 189 RQNSNIPEYLIFFSNRYIRNLTTDGSYSYLLOGL 223

RESULT 10
T42737
gp330 protein precursor - rat
N/Alternate names: megalin
C/Species: Rattus norvegicus (Norway rat)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
A/Accession: T42737
R/Saito, A.; Pietromaco, S.; Loo, A.K.C.; Faruqi, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A/Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-4660/Product: gp330 protein #status predicted <MAT>
A/Accession: T42737
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-4660 <SNI>
A/Cross-references: EMBL:L34049; NID:9561852; PID:9561853; PIDN:AAA51369.1
A/Experimental source: Strain Sprague-Dawley; Kidney
A/Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-4660/Product: gp330 protein #status predicted <MAT>

Query Match 9.0%; Score 82; DB 2; Length 4660;
Best Local Similarity 25.8%; Pred. No. 63;
Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

Qy 33 SCPEBOY-WDPULGTGCMCKTICNHQ---SQTCAAFGRSLSCRKEGKPYDH----- 81
Db 3076 TCFPHQFPCDN--GHCIEKGRVCHNHVDDCSNDSDEKGGICNECLDSSISRCDHCTDTIT 313
Qy 82 -----LNRDCTICASI--CGQHPKOCATPCENKLRSPV-NLPPELRQRSGEVE 127
Db 3134 SFYSCGLPGYKLMDSKRCVDIDECKESPQLCSQKCEVNVGSYICKCAPGYIREPDGKSC 3133
Qy 128 NNSDN-----SGRY--QGLEHRSSEASPALPGL 153
Db 3194 RQNSNIPEYLIFFSNRYIRNLTTDGSYSYLLOGL 3228

RESULT 11
JH0609
protein-tyrosine-phosphatase (EC 3.1.3.48) p19 - mouse
N/Alternate names: protein-tyrosine-phosphatase PTPY43
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A/Accession: JH0609; PS0365; PS0366; G61180
R/Iden Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijter, W.
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A/Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
A/Reference number: JH0609; MUID:92272714; PMID:1590786

A/Accession: JH0609
A/Molecule type: mRNA
A/Residues: 1-773 <DEN>
A/Cross-references: GB:K63440; GB:S36169; NID:9416181; PIDN:CAA45037.1; PID:9416182
A/Experimental source: embryonic carcinoma cell, p19 cell
A/Accession: PS0365
A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA
A/Residues: 88-91, 'G', '93-110', 'G', '112-118', 'S', '120', 'T', '122' <DE2>
A/Experimental source: embryonic carcinoma cell, p19 cell, clone PTP33
A/Accession: PS0369
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 88-91, 'G', '93-109', 'IG', '112-120', 'T', '122' <DE3>
A/Experimental source: embryonic carcinoma cell, p19 cell, clone PTP59
A/Accession: PS0366
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 88-91, 'KV', '94-109', 'IA', '112-118', 'S', '120-122' <DE4>
A/Experimental source: embryonic carcinoma cell, p19 cell, clone PTP42
R/Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A/Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells b
A/Reference number: A61180; MUID:92032882; PMID:1932742
A/Accession: G61180
A/Status: not compared with conceptual translation

A/Molecule type: mRNA
A/Residues: 124-127, 'I', '129-229' <YIA>
C/Comment: This protein is located in the cytoplasm.
C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosphatase
F/55-299/Domain: phosphoric monoester hydrolase; tyrosine-specific phosphatase
F/58-282/Domain: protein-tyrosine-phosphatase domain #status predicted <PCD>
F/337/Active site: Cys (phosphotyrosine intermediate) #status predicted
F/337/Binding site: substrate phosphate (Arg) #status predicted

Query Match 8.9%; Score 81; DB 1; Length 773;
Best Local Similarity 25.4%; Pred. No. 16;
Matches 45; Conservative 18; Mismatches 48; Indels 66; Gaps 11;

Qy 37 EOYWDPLG---TCMCKTICNHQSQTCAAFGRS--LSCKRKEGKPY-----DH- 81
Db 144 ERYW-PLYGEDPTPAFKISCENQOAR-DYFIRTLLEFONESRRRLYOFRHYWMPDHD 201
Qy 82 -----LNRD-----CISCAISGQHPKOCATPCENKLR-----S 110
Db 202 VPSSFDILDMISLMKRYOEHEDVDPICHISAGCGRTAICAIDYTNLKLXGKIPSEFN 261
Qy 111 PVNLPPELRQRSGEVE-----NNSDNGRYQGLEHRSSEASPALP 151
Db 262 VFLILQEMKQTHSAVQOTGEYELVRAIAQLFESYVOMKRF--MEHRSVVMVKLP 316

RESULT 12
I58388
protein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
A/Accession: I58388
R/Ziegler, S.F.; Bird, T.A.; Schneringer, J.A.; Schooley, K.A.; Baum, P.R.
Oncogene 8, 663-670, 1993
A/Title: Molecular cloning and characterization of a novel receptor protein tyrosine kinase
A/Reference number: I58388; MUID:93173509; PMID:8382358
A/Accession: I58388
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-1124 <RSS>
A/Cross-references: GB:L06139; NID:9292823; PIDN:AAA61139.1; PID:9292824
C/Genetics:
A/Genes: GDB:TEK
A/Cross-references: GDB:344185; OMIM:600221
A/Map position: 9p21-9p21
C/Function:

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us-09-855-158-15.rpr

Page 6

QY 132 NSGRYQGLEHRSSE 145
| : | : | :
Db 167 NQWQYGGYNQGNQ 180

Search completed: January 7, 2003, 09:41:18
Job time : 31.7143 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 12.4812 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-15

Perfect score: 909
Sequence: 1 MSGLGRSRGGRSRVDQER.....SPALPGLKSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	100.0	293	T13X_HUMAN	O14836 homo sapien
2	419.5	46.1	249	T13X_MOUSE	O98t35 mus musculu
3	97.5	10.7	1877	PK5_MOUSE	O04592 mus musculu
4	89	9.8	867	YMA2_CAEEL	P34447 caenorhabdi
5	86	9.5	297	XEDA_HUMAN	Q9hav5 homo sapien
6	83	9.1	971	RECK_MOUSE	Q920j1 mus musculu
7	83	9.1	1150	APMU_FIG	P12021 sus scrofa
8	82.5	9.1	913	PK5_HUMAN	Q92824 homo sapien
9	82	9.0	4660	LRP2_RAT	P98158 rattus norv
10	81	8.9	971	RECK_HUMAN	O95980 homo sapien
11	81	8.9	1124	TIE2_HUMAN	Q02763 homo sapien
12	80.5	8.9	937	PA4_RAT	Q02763 homo sapien
13	79.5	8.7	1172	LM3_HUMAN	Q13751 homo sapien
14	79.5	8.7	1984	YL_DROME	P98163 drosophila
15	78.5	8.6	630	Z147_HUMAN	Q14258 homo sapien
16	77.5	8.5	2871	FBN1_MOUSE	Q61554 mus musculu
17	76.5	8.4	1680	FUR2_DROME	P30432 drosophila
18	76	8.4	603	CPA1_MOUSE	Q61129 mus musculu
19	76	8.4	1877	PK5_RAT	P41413 rattus norv
20	75.5	8.3	427	YK75_YEAST	P36046 saccharomyc
21	75	8.3	400	LM6_HIRME	Q25092 hircudo medi
22	75	8.3	446	FA7_MOUSE	P70375 mus musculu
23	75	8.3	448	EDAF_HUMAN	O9ure0 homo sapien
24	75	8.3	969	PA4_HUMAN	P29122 homo sapien
25	75	8.3	2871	FBN1_HUMAN	P35555 homo sapien
26	75	8.3	4544	LRN1_HUMAN	Q07954 homo sapien
27	74.5	8.2	501	TRAI_MOUSE	P39429 mus musculu
28	74.5	8.2	773	TIE2_BOVIN	P53712 bos taurus
29	74	8.1	1125	TIE2_BOVIN	Q06807 bos taurus
30	74	8.1	1426	EGFR_DROME	P04412 drosophila
31	74	8.1	2569	LM3_MOUSE	Q61789 mus musculu
32	73.5	8.1	775	PTNC_MOUSE	P35831 mus musculu
33	73.5	8.1	798	ITB1_MOUSE	P09055 mus musculu

34	73.5	8.1	1693	1	RIP2_MOUSE	P97433 mus musculu
35	73	8.0	61	1	MTID_FIG	P79377 sus scrofa
36	73	8.0	4393	1	PGEM_HUMAN	P98160 homo sapien
37	72.5	8.0	450	1	NH14_CAEEL	O02151 caenorhabdi
38	72.5	8.0	634	1	2147_MOUSE	O61510 mus musculu
39	72.5	8.0	780	1	PTNC_HUMAN	Q05209 homo sapien
40	72.5	8.0	788	1	ITB6_HUMAN	P18564 homo sapien
41	72.5	8.0	1696	1	PK5_BRACL	Q9nj15 branchiosto
42	72	7.9	290	1	HXD8_HUMAN	P13378 homo sapien
43	72	7.9	308	1	ACPI_ENTHI	P36184 entamoeba h
44	72	7.9	354	1	VEGD_HUMAN	O43915 homo sapien
45	72	7.9	448	1	EDAR_MOUSE	Q9r187 mus musculu

ALIGNMENTS

RESULT 1
T13X_HUMAN
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC O14836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE=B-Cell;
RX MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
[2]
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN FUNCTION
MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLys.";
RL J. Biol. Chem. 275:35478-35485(2000).
[4]
RN FUNCTION
MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
CC -!
CC -! FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates cell function and the regulation of humoral immunity.
CC -! SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal domain of CAMLg with its C-terminus.
CC -! SUBCELLULAR LOCATION: Type III membrane protein.
CC -! TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting B-

cells and activated T-cells, but not in resting T-cells.

CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.

CC -----

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CC -----

DR EMBL; AF023614; AAC51790.1; -

DR EMBL; BC028072; AAH2807.1; -

DR Genew; HGNC:18153; TNFRSF13B.

DR MIM; 604907; -

DR InterPro; IPR001368; TNFR_C6.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00650; TNFR_NGFR_2; FALSE NEG.

KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;

KW Repeat.

FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)

FT REPEAT 187 293 (POTENTIAL).

FT REPEAT 33 67 CYTOPLASMIC (POTENTIAL).

FT DISULFID 70 104 TNFR-CYS 1.

FT DISULFID 34 47 TNFR-CYS 2.

FT DISULFID 50 62 BY SIMILARITY.

FT DISULFID 54 66 BY SIMILARITY.

FT DISULFID 71 86 BY SIMILARITY.

FT DISULFID 89 100 BY SIMILARITY.

FT DISULFID 93 104 BY SIMILARITY.

FT CARBOHD 128 128 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHD 251 251 P -> L (IN REF. 2).

FT SEQUENCE 293 AA; 31816 MW; 4117993DE17A5EB CRC64;

Query Match 100.0%; Score 909; DB 1; Length 293;

Best Local Similarity 100.0%; Pred. No. 4,3e-79;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRGRGRGRVDOERPPQGLMTGVAMRSCEPEQYWDLLGTGMSCKTICNHQSQR 60

DB 1 MSGLSRGRGRGRVDOERPPQGLMTGVAMRSCEPEQYWDLLGTGMSCKTICNHQSQR 60

QY 61 TCAAFCRSLSCREKQGFYDHLRLDPCISCAISCGQHPKQCAFCENKLRSPVNLPEELR 120

DB 61 TCAAFCRSLSCREKQGFYDHLRLDPCISCAISCGQHPKQCAFCENKLRSPVNLPEELR 120

QY 121 QRSGEVENNSDNGRYQGLEHRSSEASPLPGLKLSADQVALVYST 166

DB 121 QRSGEVENNSDNGRYQGLEHRSSEASPLPGLKLSADQVALVYST 166

RESULT 2

113X_MOUSE STANDARD; PRT; 249 AA.

AC Q9ET35; Q9DBZ3; -

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane

DE activator and CAML interactor).

GN TNFRSF13B OR TACI.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI Taxid=10090;

RX NCB1_Taxid=10090;

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=21177254; PubMed=10881172;

FT Yan M., Masters S.A., Grewal I.S., Wang H., Ashkenazi A.,

RA Dixit V.M.;

RT "Identification of a receptor for Blys demonstrates a crucial role in

RT humoral immunity.";

RL Nat. Immunol. 1:37-41(2000).

RV [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

RA Altwegg K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Schirrl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,

RA Sakai K., Boffelli D., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Noridone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RV Nature 409:685-690(2001).

RV [3]

RP FUNCTION

RX MEDLINE=20341628; PubMed=10880535;

RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,

RA Theill L.E., Colomero A., Solovay I., Lee F., McCabe S., Elliott R.,

RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,

RA Weng S.-Y., Boyle W.J., Han H.;

RT "TRAC1 is a TRAF-interacting receptor for TAU-1, a tumor necrosis

RT factor family member involved in B cell regulation.";

RL J. Exp. Med. 192:137-143(2000).

RV [4]

RP FUNCTION

RX MEDLINE=21322748; PubMed=11429548;

RA Wang H., Masters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,

RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;

RT "TRAC1-ligand interactions are required for T cell activation and

RT collagen-induced arthritis in mice.";

RL Nat. Immunol. 2:632-637(2001).

CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TRA1/BAFF/Blys

CC that binds both ligands with similar high affinity. Mediates

CC calcineurin-dependent activation of NF-AT, as well as activation

CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-

CC cell function and the regulation of humoral immunity (by

CC similarity).

CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal

CC domain of CAML with its C-terminus (by similarity).

CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

CC -----

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CC -----

DR EMBL; AF57673; AAC00081.1; -

DR EMBL; AK004668; BAB23457.1; -

DR MGD; MGI:1889411; Tnfrcf13b.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00650; TNFR_NGFR_2; 2.

KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.

FT DOMAIN 1 128 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 129 149 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)


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FT DOMAIN 150 249 (POTENTIAL).
FT REPEAT 5 38 TNFR-CYS 1.
FT REPEAT 42 76 TNFR-CYS 2.
FT DISULFID 6 19 BY SIMILARITY.
FT DISULFID 22 34 BY SIMILARITY.
FT DISULFID 26 38 BY SIMILARITY.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 65 76 BY SIMILARITY.
FT CONFLICT 137 137 I -> F (IN REF. 2). CRC64;
SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 46.1%; Score 419.5; DB 1; Length 249;
Best Local Similarity 55.1%; Pred. No. 8.6e-33;
Matches 76; Conservative 22; Mismatches 31; Indels 9; Gaps 2;

OY 29 VAMRSCPEQYWDPLGLTGMCKTICNHQSORTCAAFCSLSCKRQKGFYDHLRLDCIS 88
Db 1 MAMAFPCPKDQYWDSSRKSCVSCALTCQSRSORTCTDFCKFINCRKEQGRYYDHLHGACVS 60
OY 89 CASICQHPKQCAFCENKLRSPVNLPELRRQSRGVEVNSDNGRYQGLEHGRGSEASP 148
Db 61 CDSCTCTHPQCAHFCRPRSQANLQPELGRPOAGEVEVRSDNSGRHGSSEHG----- 114
OY 149 ALPGLKLSADQVALVYST 166
Db 115 --PGLRLSSDQLTL-YCT 129

RESULT 3
PKCS_MOUSE STANDARD; PRT; 1877 AA.
ID FCX_MOUSE
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protease convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Proteinase convertase PC5) (Subtilisin/kexin-like protease PC5)
DE (Convertase PC5) (PC6) (subtilisin-like proteinase convertase 6)
DE (SPC6).
GN PC5K5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).
RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM PC5A).
RC TISSUE=Brain, and Intestine;
RX MEDLINE=93224489; PubMed=8468318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.;
RA Nakayama K.;
RT "Identification and functional expression of a new member of the
mammalian Kex2-like processing endoprotease family: its striking
structural similarity to PACE4.";
RL J. Biochem. 113:132-135(1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM PC5A).
RC TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
RT "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate protease convertase expressed in endocrine and
nonendocrine cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
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RN PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97103178; PubMed=8947550;
RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
RA Bendayan M., Seidah N.G.;
RT "The isoforms of proprotein convertase PC5 are sorted to different
subcellular compartments";
RL J. Cell Biol. 135:1261-1275(1996).
RN [5]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=96293359; PubMed=8698813;
RA Constam D.B., Galfon M., Robertson E.J.;
RT morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
RN [6]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=97436919; PubMed=9291583;
RA Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
CC -!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
OF GROWTH FACTORS.
CC -!- CATALYTIC ACTIVITY. RELEASE OF MATURE PROTEINS FROM THEIR
PROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC -!- SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED
SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
EARLY ENDOSOMES.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PC5B/LONG (SHOWN HERE)
AND PC5A/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: PC5A IS EXPRESSED IN MOST TISSUES BUT IS MOST
ABUNDANT IN THE INTESTINE AND ADRENALS. PC5B IS EXPRESSED IN THE
INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
CC -!- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN
E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
CC -!- ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
ISOFORM B OCCUR AT E12.5
CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
ASSISTING THE FOLDING OF THE ZIMOGEN WITHIN THE ENDOPLASMIC
RETICULUM.
CC -!- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
WITH THE TGN SORTING PROTEIN PACS-1.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
CC -!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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EMBL; D17583; BAA04507.1; -.
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DR EMBL: D12619; BAA02143.1; -
DR EMBL: L14932; AAT74636.1; -
DR PIR: JX0225; JX0248.
DR PIR: A48225; A48225.
DR HSP: Q99405; IMPT.
DR MEROPS: S08.076; -.
DR MGD: MG1.97515; Pex5.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002884; P_domain.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam: PF00082; Peptidase_S8; 1.
DR Pfam: PF01483; P; PARTIAL.
DR PRINTS: PR00723; SUBTILISIN.
DR ProDom: PD000717; P_domain; 1.
DR SMART: SM00181; EGF; 3.
DR SMART: SM00261; FU; 2.
DR PROSITE: PS00136; SUBTILASE ASP; 1.
DR PROSITE: PS00137; SUBTILASE HIS; 1.
DR PROSITE: PS00138; SUBTILASE SER; 1.
DR Hydrolase: Serine protease; Zymogen; Signal;
KW Cleavage on pair of basic residues; Repeat; Alternative splicing;
KW Transmembrane.
KT SIGNAL 1 34
KT PROPEP 35 116
KT CHAIN 117 1877
FT DOMAIN 117 1768
FT TRANSFEM 1179 1788
FT DOMAIN 1179 1877
FT DOMAIN 1179 1877
FT DOMAIN 117 452
FT DOMAIN 464 602
FT DOMAIN 638 1753
FT DOMAIN 1825 1844
FT DOMAIN 1856 1877
FT SITE 116 117
FT SITE 521 523
FT ACT_SITE 173 173
FT ACT_SITE 214 214
FT ACT_SITE 368 368
FT CARBOHYD 227 227
FT CARBOHYD 383 383
FT CARBOHYD 667 667
FT CARBOHYD 754 754
FT CARBOHYD 804 804
FT CARBOHYD 854 854
FT CARBOHYD 951 951
FT CARBOHYD 1016 1016
FT CARBOHYD 1220 1220
FT CARBOHYD 1317 1317
FT CARBOHYD 1523 1523
FT CARBOHYD 1711 1711
FT CARBOHYD 1733 1733
FT VARSPLIC 878 915
FT VARSPLIC 916 1877
FT VARSPLIC 1877 1877
SQ SEQUENCE 1877 AA; 209287 MW; EC850E2DF20EALC3 CRC64;
Query Match 10.7%; Score 97.5; DB 1; Length 1877;
Best Local Similarity 30.2%; Pred. No. 0.21;
Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

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RESULT 4
VW2A CAPEL STANDARD: PRT; 867 AA.
ID VW2A CAPEL
AC P34417.P34448;
DI 1-SEP-1994 (Rel. 28, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DI Hypothetical protein F54F2.2 in chromosome III, isoform a.
GN F54F2.2/F54F2.3/F54F2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Pavelle A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnson L., Jones M., Kershaw J., Kirsten J., Laisner N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roodra A., Saunders D., Showkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Weinstock L.,
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RA elegans.
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RL Submitted (MAR 2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b (AC
CC P34449); may be produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 2 PHD ZINC-FINGER DOMAINS.
CC -----
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CC -----
CC EMBL: L23645; AAK26137.1; -.
DR PIR: S44827; S44827.
DR WormPep: F54F2.2; CE25003.
DR InterPro: IPR001965; Znf_PHD.
DR Pfam: PF00628; PHD; 1.
DR SMART: SM00249; PHD; 2.
KM Hypothetical protein; Metal-binding; Zinc; Zinc-finger; Repeat;
KM DNA-binding; Nuclear protein; Alternative splicing.
FT ZN_FING 5 57
FT ZN_FING 124 185
FT ZN_FING 124 185
SQ SEQUENCE 867 AA; 92189 MW; 7E582DC529CFEAD CRC64;
Query Match 9.8%; Score 89; DB 1; Length 867;
Best Local Similarity 32.5%; Pred. No. 0.61;
Matches 27; Conservative 8; Mismatches 28; Indels 20; Gaps 5;

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RESULT 5
XEDA HUMAN
ID XEDA HUMAN STANDARD; PRT; 297 AA.
AC Q9HAV5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member XEDAR (X-linked
DE ectodysplasin-A2 receptor) (EDA-A2 receptor).
GN XEDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF GLU-256.
RC TISSUE=Fetal kidney;
RX MEDLINE=20495245; PubMed=11039935;
RA Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RA de Vos A.M., Gao W.-Q., Dixit V.M.;
RT "Two-amino acid molecular switch in an epithelial morphogen that
RT regulates binding to two distinct receptors.";
RL Science 290:523-527(2000).
CC -!- FUNCTION: Receptor for EDA isoform A2, but not for EDA isoform
CC A1. Mediates the activation of NF-kappa-B. Activation seems to
CC be mediated by binding to TRAF6.
CC -!- SUBUNIT: Associates with TRAF1, TRAF3 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; AF298812; AAG28761.1; -.
CC MIM; 300276; -.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00650; TNFR_NGFR_2; 2.
CC Receptor; Developmental protein; Differentiation; Transmembrane;
CC Glycoprotein; Repeat.
CC DOMAIN 1 138 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 139 159 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
CC
CC DOMAIN 160 297 CYTOPLASMIC (POTENTIAL).
CC REPEAT 2 41 TNFR-CYS 1.
CC REPEAT 43 83 TNFR-CYS 2.
CC REPEAT 85 118 TNFR-CYS 3.
CC DISULFID 18 31 BY SIMILARITY.
CC DISULFID 21 41 BY SIMILARITY.
CC DISULFID 44 58 BY SIMILARITY.
CC DISULFID 61 75 BY SIMILARITY.
CC DISULFID 84 104 BY SIMILARITY.
CC DISULFID 86 104 BY SIMILARITY.
CC DISULFID 107 118 BY SIMILARITY.
CC CARBOHYD 74 74 N-LINKED (GLCNAC... ) (POTENTIAL).
CC MUTAGEN 256 256 E->R: ABOLISHES TRAF6 ASSOCIATION.
CC SEQUENCE 297 AA; 32728 MW; 0E71127C6C48240C CRC64;
Query Match 9.5%; Score 86; DB 1; Length 297;
Best Local Similarity 22.0%; Pred. No. 0.4;
Matches 26; Conservative 19; Mismatches 31; Indels 42; Gaps 7;
34 CPFEQYWDPLLLGTCMSCKTIC--NHQSQRTCA-----AFCRSLSCRKBOGKFYDHLRLD 85
3 COENEYWDQ-WGRCVTCQR-CGPGQELSKDCGVGGGDVACTACPPRYKSSWGHRCQS 60
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QY 86 CISCA-----SICGHPKQCAFCENKLRSPVLPPELRORSCEVEN 128
DB 61 CITCAVINRVQKVNCTATSNVCGD-----C-----LPRFYRKTRIGLQD 101

RESULT 6
RECK_MOUSE
ID RECK_MOUSE STANDARD; PRT; 971 AA.
AC Q9Z0J1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor
DE (mRECK).
DE
GN RECK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
RT invasion by the membrane-anchored glycoprotein RECK.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
CC by suppressing MMP-9 secretion, and by direct inhibition of its
CC enzymatic activity. RECK down-regulation by oncogenic signals may
CC facilitate tumor invasion and metastasis. Appears to also
CC regulate MMP-2 and Mti-MMP, which are involved in cancer
CC progression (By similarity).
CC -!- SUBUNIT: Interacts with MMP-9.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- DEVELOPMENTAL STAGE: In E10.5 embryos the RECK protein is widely
CC expressed in mesenchymal tissues and is relatively abundant in the
CC marginal zone of the neural tube and large blood vessels such as
CC the aorta.
CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB006960; BAA34061.1; -.
CC MCD; MG1.1855698; Reck.
CC InterPro; IPR002350; Kazal.
CC Pfam; PF00050; Kazal; 2.
CC SMART; SM00280; KAZAL; 2.
CC PROSITE; PS00282; KAZAL; 1.
CC Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
CC Membrane; Anti-oncogene; Repeat.
CC CHAIN 1 22 POTENTIAL.
CC SIGNAL 23 942 WITH KAZAL MOTIFS.
CC REVERSION-INDUCING CYSTEINE-RICH PROTEIN
CC WITH KAZAL MOTIFS.
CC REMOVED IN MATURE FORM (POTENTIAL).
CC GPI-ANCHOR (POTENTIAL).
CC KAZAL-LIKE 1.
CC KAZAL-LIKE 2 (DEGENERATE).
CC KAZAL-LIKE 3 (DEGENERATE).
CC 5 X KNOT REPEATS.
CC KNOT 1.
CC KNOT 2.
CC KNOT 3.
CC KNOT 4.
CC KNOT 5.
CC REPEAT 943 971
CC REPEAT 942 942
CC REPEAT 633 677
CC REPEAT 704 750
CC REPEAT 751 787
CC REPEAT 37 338
CC REPEAT 37 84
CC REPEAT 104 141
CC REPEAT 151 197
CC REPEAT 216 263
CC REPEAT 292 338
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FT CARBOHYD 96 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 98 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 101 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 103 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 104 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 106 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 107 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 108 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 110 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 111 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 112 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 113 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 114 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 117 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 123 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 124 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 148 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 547 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 547 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 917 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 985 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1002 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1068 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 1150 AA; 109615 MW; 3CB68B5D29DD7F5A CRC64;

Query Match 9.1%; Score 83; DB 1; Length 1150;
Best Local Similarity 23.5%; Pred. No. 3;
Matches 32; Conservative 18; Mismatches 44; Indels 42; Gaps 8;

OY 18 ERFPGGLTGVAMR-SCPEQVWD-----PLLGTCMCKTICNHOSORTCAAFCSLS 70
Db 937 EKSQPGVMTWANCHKCTCTEAKTVCKPCPSPPCKTGERLKFKANDTC--CEIGH 993
OY 71 CRK-----EKGKFDHLLRDCI--SCASI-----CGOH-----PKO 99
Db 994 CEKRTCLFNNTDYEVSFDDPNPNCTVTSQNTGFTAVVQNCPKTWCABEDRVDSKQ 1053
OY 100 CAYFCENKLR-SPVNL 114
Db 1054 CQYCKSSCKPSPVNV 1069

RESULT 8
PKCS HUMAN
ID PKCS HUMAN STANDARD; PRT; 913 AA.
AC Q92824; Q13527;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Protein convertase PCS) (Subtilisin/kexin-like protease PCS)
DE (Convertase PCS) (PCS) (hPC6).
GN PKCS5 OR PCS OR PC6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=csl;
RX MEDLINE=9635380; PubMed=875538;
RA Miranda L., Wolf J., Pichuanes S., Duke R., Franzusoff A.;
RT "Isolation of the human PC6 gene encoding the putative host protease
for HIV-1 gp160 processing in CD4+ T lymphocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
RN [2]
RP REVISIONS.
RA Franzusoff A., Miranda L., Wolf J., Pichuanes S., Lu Y., Duke R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 15-913 FROM N.A.
RA Reudelhuber T.L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
CC OF CLEAVAGE AT THE RX(K/R) CONSENSUS MOTIF.
CC -!- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR

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CC PROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEMS TO BE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN T-LYMPHOCYTES.
CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
CC RETICULUM. BELONGS TO PEPTIDASE FAMILY S8.
CC -!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; U56387; AAC50643.2; -
CC EMBL; U49114; AAA91807.1; -
CC HSSP; Q99405; IMPT.
CC MEROPS; S08.076; -
CC Genew; HGNC:8747; PCSK5.
CC
CC MW: 600488;
CC InterPro: IPR002174; Furin-like.
CC InterPro: IPR002884; P domain.
CC InterPro: IPR002029; Peptidase S8.
CC Pfam; PF00082; Peptidase S8; 1.
CC Pfam; PF01483; P; PARTIAL.
CC PRINTS; PR00723; SUBTILISIN.
CC PRODOM; PD000717; F_domain; 1.
CC SMART; SM00261; FU; 5.
CC PROSITE; PS00136; SUBTILASE ASP; 1.
CC PROSITE; PS00137; SUBTILASE HIS; 1.
CC PROSITE; PS00138; SUBTILASE SER; 1.
CC Hydrolase; Serine protease; Glycoprotein; Zymogen; signal;
CC Cleavage on pair of basic residues; Repeat.
CC SIGNAL 1 32
CC BY SIMILARITY.
CC PROPEP 33 114
CC PROTEIN CONVERTASE SUBTILISIN/KEXIN
CC CHAIN 115 913
CC TYPE 5.
CC
CC CATALYTIC.
CC DOMAIN 115 454
CC HOMO B.
CC CYS-RICH MOTIF (CRM) REGION.
CC CLEAVAGE (AUTO-) (BY SIMILARITY).
CC CELL ATTACHMENT SITE (POTENTIAL).
CC CHARGE RELAY SYSTEM (BY SIMILARITY).
CC CHARGE RELAY SYSTEM (BY SIMILARITY).
CC CHARGE RELAY SYSTEM (BY SIMILARITY).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC S -> F (IN REF. 3).
CC V -> A (IN REF. 3).
CC R -> A (IN REF. 3).
CC R -> Q (IN REF. 3).
CC SIGNAL 601 601
CC SEQUENCE 913 AA; 101775 MW; 21389264CAD7546C CRC64;
CC
Query Match 9.1%; Score 82.5; DB 1; Length 913;
Best Local Similarity 26.0%; Pred. No. 2.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
OY 27 TGVAMRSCPEQYWDPLLGTCMCKTICNHOSORTCAAF-----CR-----SLSC 71
Db 717 TNSCVTHCPDGSQYDTKKNLCRKCSENC-----KTCTEFHNCTECRDGLSLQSGRCVSC 771
OY 72 RKEGKFDHLLRDCISASCIC-----GOHPKQC-----AYECEN 106

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2479 2518 LDL-RECEPTOR CLASS B 26.
 FT DOMAIN 2520 LDL-RECEPTOR CLASS B 27.
 FT DOMAIN 2564 LDL-RECEPTOR CLASS B 28.
 FT DOMAIN 2604 LDL-RECEPTOR CLASS B 29.
 FT DOMAIN 2652 EGF-LIKE 10.
 FT DOMAIN 2694 LDL-RECEPTOR CLASS A 16.
 FT DOMAIN 2739 LDL-RECEPTOR CLASS A 17.
 FT DOMAIN 2778 LDL-RECEPTOR CLASS A 18.
 FT DOMAIN 2820 LDL-RECEPTOR CLASS A 19.
 FT DOMAIN 2862 LDL-RECEPTOR CLASS A 20.
 FT DOMAIN 2903 LDL-RECEPTOR CLASS A 21.
 FT DOMAIN 2947 LDL-RECEPTOR CLASS A 22.
 FT DOMAIN 2988 LDL-RECEPTOR CLASS A 23.
 FT DOMAIN 2993 LDL-RECEPTOR CLASS A 24.
 FT DOMAIN 3032 LDL-RECEPTOR CLASS A 25.
 FT DOMAIN 3075 EGF-LIKE 11.
 FT DOMAIN 3153 EGF-LIKE 12.
 FT DOMAIN 3194 LDL-RECEPTOR CLASS B 30.
 FT DOMAIN 3241 LDL-RECEPTOR CLASS B 31.
 FT DOMAIN 3284 LDL-RECEPTOR CLASS B 32.
 FT DOMAIN 3335 LDL-RECEPTOR CLASS B 33.
 FT DOMAIN 3379 LDL-RECEPTOR CLASS B 34.
 FT DOMAIN 3421 EGF-LIKE 13.
 FT DOMAIN 3467 LDL-RECEPTOR CLASS A 26.
 FT DOMAIN 3512 LDL-RECEPTOR CLASS A 27.
 FT DOMAIN 3553 LDL-RECEPTOR CLASS A 28.
 FT DOMAIN 3594 LDL-RECEPTOR CLASS A 29.
 FT DOMAIN 3635 LDL-RECEPTOR CLASS A 30.
 FT DOMAIN 3678 LDL-RECEPTOR CLASS A 31.
 FT DOMAIN 3719 LDL-RECEPTOR CLASS A 32.
 FT DOMAIN 3759 LDL-RECEPTOR CLASS A 33.
 FT DOMAIN 3798 LDL-RECEPTOR CLASS A 34.
 FT DOMAIN 3842 LDL-RECEPTOR CLASS A 35.
 FT DOMAIN 3883 LDL-RECEPTOR CLASS A 36.
 FT DOMAIN 3928 EGF-LIKE 14.
 FT DOMAIN 3968 EGF-LIKE 15.
 FT DOMAIN 4009 LDL-RECEPTOR CLASS B 35.
 FT DOMAIN 4196 LDL-RECEPTOR CLASS B 36.
 FT DOMAIN 4244 LDL-RECEPTOR CLASS B 37.
 FT DOMAIN 4284 EGF-LIKE 16.
 FT DOMAIN 4332 EGF-LIKE 17.
 FT DOMAIN 4379 SH3-BINDING (POTENTIAL).
 FT SITE 4454 SH3-BINDING (POTENTIAL).
 FT SITE 4457 SH2-BINDING (POTENTIAL).
 FT SITE 4606 SH3-BINDING (POTENTIAL).
 FT SITE 4619 SH3-BINDING (POTENTIAL).
 FT SITE 4624 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 1743 ENDOCYTOSIS SIGNAL (POTENTIAL).
 FT SITE 1745 ENDOCYTOSIS SIGNAL (POTENTIAL).
 FT SITE 4522 BY SIMILARITY.
 FT SITE 4601 BY SIMILARITY.
 FT DISULFID 28 BY SIMILARITY.
 FT DISULFID 35 BY SIMILARITY.
 FT DISULFID 47 BY SIMILARITY.
 FT DISULFID 67 BY SIMILARITY.
 FT DISULFID 74 BY SIMILARITY.
 FT DISULFID 87 BY SIMILARITY.
 FT DISULFID 108 BY SIMILARITY.
 FT DISULFID 115 BY SIMILARITY.
 FT DISULFID 127 BY SIMILARITY.
 FT DISULFID 147 BY SIMILARITY.

Query Match 9.0%; Score 82; DB 1; Length 4660;
 Best Local Similarity 25.8%; Pred. No. 15;
 Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

QY 33 SCPEEQY-WDPLGLGCMCKTICNHQ---SQTCAAFRCFLSCRKCEQGFYDH-----81
 DB 3076 TCFPHQFRCDN--GHCIEGRVNCVHVDGSDNSDEKGCINECLDSSISRCDCNCTDTIT 3133
 QY 82 -----LLRDCISCAST--CGQHPKQCAFCENKLRSPV-NLPDLRRQSSGEVE 127
 DB 3134 SFVCSCLPGYKLMDSKRSVDIDECKESQQLCSQKCNVGVSVICKCAPGYREPDKSC 3193
 QY 128 NNSDN-----SGRY-QGLEHRGSEASPALPGL 153

Db 3194 RQNSNIEPYLFISNRYIRNLTTDGSYSVLQLQL 3228
 RESULT 10
 RECK_HUMAN STANDARD; PRT; 971 AA.
 AC O95980; OSWK37;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor
 DE (hRECK) (Suppressor of tumorigenicity 15) (STI15).
 GN RECK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND N-GLYCOSYLATION.
 RC TISSUE=Fibroblast;
 RX MEDLINE=99007295; PubMed=9789069;
 RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
 RA Kitaura Y., Takai S., Saishara R.M., Horimoto A., Ikawa Y.,
 RA Ratzkin B.J., Arakawa T., Noda M.;
 RT Regulation of matrix metalloproteinase-9 and inhibition of tumor
 invasion by the membrane-anchored glycoprotein RECK.;
 RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
 RN [2]
 RP SEQUENCE OF 363-971 FROM N.A.
 RA Kimberley A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
 CC by suppressing MMP-9 secretion and by direct inhibition of its
 CC enzymatic activity. RECK down-regulation by oncogenic signals may
 CC facilitate tumor invasion and metastasis. Appears to also
 CC regulate MMP-2 and MT1-MMP, which are involved in cancer
 CC progression.
 CC -!- SUBUNIT: Interacts with MMP-9.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Expressed in various tissues and untransformed
 CC cells. It is undetectable in tumor-derived cell lines and
 CC oncogenically transformed cells.
 CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
 CC
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 EMBL; D50406; BAA34050.1; --
 EMBL; AL158850; CAD13384.1; --
 Genew; HGNC:11345; RECK.
 MIM; 605227; --
 HSP; P80424; IAN1.
 InterPro; IPR002350; Kazal.
 SMART; SM00280; KAZAL; 3.
 SMART; SM00011; VWC Def; 1.
 PROSITE; PS00282; KAZAL; 1.
 Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
 Membrane; Anti-oncogene; Repeat.
 SIGNAL 1 22
 CHAIN 23 942
 REVERSION-INDUCING CYSTEINE-RICH PROTEIN
 WITH KAZAL MOTIFS.
 FT PROPEP 943 971 GPI-ANCHOR (POTENTIAL).
 FT LIPID 942 942 KAZAL-LIKE 1.
 FT DOMAIN 632 677 KAZAL-LIKE 2 (DEGENERATE).
 FT DOMAIN 708 750 KAZAL-LIKE 3 (DEGENERATE).
 FT DOMAIN 753 787 5 X KNOT REPEATS.
 FT DOMAIN 37 338

FT REPEAT 37 84 KNOT 1.
 FT REPEAT 104 141 KNOT 2.
 FT REPEAT 151 197 KNOT 3.
 FT REPEAT 216 263 KNOT 4.
 FT REPEAT 292 338 KNOT 5.
 FT DISULFID 635 654 BY SIMILARITY.
 FT DISULFID 633 658 BY SIMILARITY.
 FT DISULFID 633 677 BY SIMILARITY.
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 971 AA; 106456 MW; 173D47D6A8E6F834 CRC64;

Query Match 8.9%; Score 81; DB 1; Length 971;
 Best Local Similarity 21.8%; Pred. No. 3.9;
 Matches 32; Conservative 18; Mismatches 41; Indels 56; Gaps 8;

QY 34 CPEE--QYVDP------LGTG-----MSCKTICNHQSORTCAAFCRSL 70
 DB 74 CPEIWEIWNQWNSLPGVFKKSDGNGVIGCCCLATLALBROCKQASSKNDI---SKV 129
 QY 71 CRKGGKFPYDHLRPDCTIS-----CASIGQHPKOCVAFCEKRLSPVNLPELRORS 123
 DB 130 CRKE-----YENLFSCTISNEMSGVCCSYAGHH-TMCRGYCAIFRT----- 171
 QY 124 GEVENNSDNGRGYGVGHEHSGSEAPL 150
 DB 172 ----DSSPGSPQIKAVENICASISPOL 194

RESULT 11
 TIE2_HUMAN STANDARD; PRT; 1124 AA.
 ID TIE2_HUMAN
 AC 002763;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 15-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-UN-2002 (Rel. 41, Last annotation update)
 DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (P140
 DE TEK) (human internal endothelial cell kinase) (CD202b antigen).
 GN TEK OR TIE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=93173509; PubMed=8382358;
 RA Ziegler S.F., Bird T.A., Scherzinger J.A., Schooley K.A., Baum P.R.,
 RT "Molecular cloning and characterization of a novel receptor protein
 RT tyrosine kinase from human placenta.",
 RL Oncogene 8:663-670(1993).
 RN [2]
 RP VARIANT VMCW1 TRP-849.
 RX MEDLINE=97134665; PubMed=8980225;
 RA Virkula M., Boon L.M., Cartaway K.L. III, Calvert J.T., Diamond A.J.,
 RA Gummertov B., Paayk K.A., Marchuk D.A., Worman M.L., Cantley L.C.,
 RA Mulliken J.B., Olse B.R.;
 RT "Vascular dysmorphogenesis caused by an activating mutation in the
 RT receptor tyrosine kinase TIE2.",
 RL Cell 87:1181-1190(1996).
 RN [3]
 RP VARIANTS VMCW1 TRP-849 AND SER-897.
 RX MEDLINE=99299243; PubMed=10369874;
 RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
 RA Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Paayk K.A.,
 RA Speer M.C., Peters K.G., Marchuk D.A.;
 RT "Allelic and locus heterogeneity in inherited venous malformations.",
 RL Hum. Mol. Genet. 8:1279-1289(1999).
 CC -!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE

CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
 CC MAMMALIAN ENDOTHelial CELL LINEAGE MARKER. PROBABLY REGULATES
 CC ENDOTHelial CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
 CC PROPER PATTERNING OF ENDOTHelial CELLS DURING BLOOD VESSEL
 CC FORMATION.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC AND THEIR PROGENITORS, THE ANGIOBLASTS, HAS BEEN DIRECTLY FOUND
 CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
 CC ENDOTHelial CELLS, BRAIN AND KIDNEY.
 CC -!- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
 CC MALFORMATIONS (VMCW1), AN ERROR OF VASCULAR MORPHOGENESIS
 CC CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TIE
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -!- DATABASE: NAME=PROV; NOTE=PROV 3:12-14(2002);
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1715848914.g.htm".
 CC -----
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 CC -----
 CC EMBL; L06139; AAA61139.1; --
 CC HSSP; F11362; 1FGK.
 CC Genew; HSCG:11724; TEK.
 CC MIM; 600221; --
 CC MIM; 600195; --
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR001245; TYF_pkinase.
 CC Pfam; PF00008; EGF_1.
 CC Pfam; PF00041; fn3; 3.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC PRODOM; PD000001; Euk_pkinase; 1.
 CC SMART; SM00181; EGF_2.
 CC SMART; SM00001; EGF-like; 1.
 CC SMART; SM00060; FN3_3.
 CC SMART; SM00219; Tyrc; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 CC PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
 CC PROSITE; PS00022; EGF_1_3.
 CC PROSITE; PS01186; EGF_2_3.
 CC Receptor_Tyrosine-protein_kinase; Transferase; Signal; ATP-binding;
 CC Repeat_EGF-like_domain; Transmembrane; Immunoglobulin domain;
 CC Glycoprotein; Phosphorylation; Multigene family; Disease mutation.
 CC SIGNAL 1 18
 CC CHAIN 19 1124
 CC DOMAIN 19 745
 CC TRANSMEM 746 770
 CC DOMAIN 771 1124
 CC DOMAIN 44 102
 CC DOMAIN 210 252
 CC DOMAIN 254 299
 CC DOMAIN 301 341
 CC DOMAIN 370 424
 CC DOMAIN 444 536
 CC DOMAIN 541 634
 CC DOMAIN 638 732
 CC DOMAIN 824 1096
 CC NP BIND 830 838
 CC BINDING 855 855
 CC ATP (BY SIMILARITY).

RA Pulkkinen L., Gerecke D.R., Christiano A.M., Magman D.W.,
RA Burgeson R.E., Uitto J.,
RT "Cloning of the beta 3 chain gene (LAMB3) of human laminin 5, a
RT candidate gene in junctional epidermolysis bullosa.",
RL Genomics 25:192-198 (1995).
RN [21]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 172-190.
RX MEDLINE=94209274; PubMed=7512558;
RA Gerecke D.R., Magman D.W., Champilaud M.F., Burgeson R.E.;
RT "The complete primary structure for a novel laminin chain, the
RT laminin Bk chain".
RL J Biol. Chem. 269:11073-11080 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21221101; PubMed=11296269;
RA Robbins P.B., Lin O., Goodnough U.B., Tian H., Chen X., Khavari P.A.;
RT "In vivo restoration of laminin 5 beta 3 expression and function in
RT junctional epidermolysis bullosa.".
RL Proc. Natl. Acad. Sci. U.S.A. 98:5193-5198 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Epidermis;
RX MEDLINE=96015057; PubMed=8530036;
RA Morishima Y., Aiyama T., Yamashita K., Abe T., Ueda E., Yasuno H.,
RA Inazawa J.,
RT "Chromosomal loci of 50 human keratinocyte cDNAs assigned by
RT fluorescence in situ hybridization.";
RL Genomics 28:273-279 (1995).
RN [5]
RP SEQUENCE FROM N.A.
RX Grafham D.,
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
RN [6]
RP VARIANT JEB LEU-679.
RX MEDLINE=96055522; PubMed=7550237;
RA Pulkkinen L., McGrath J.A., Christiano A.M., Uitto J.;
RT "Detection of sequence variants in the gene encoding the beta 3 chain
RT of laminin 5 (LAMB3)".
RL Hum. Mutat. 6:77-84 (1995).
RN [7]
RP VARIANT GABEB LYS-210.
RX MEDLINE=99089987; PubMed=9767254;
RA Melletto U.B., Eady R.A., Atherton D.J., Lake B.D., McGrath J.A.;
RT "E210K mutation in the gene encoding the beta3 chain of laminin-5
RT (LAMB3) is predictive of a phenotype of generalized atrophic benign
RT epidermolysis bullosa.";
RL Br. J. Dermatol. 139:325-331 (1998).
CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE BETA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILGRIN/KALININ/
CC NICEIN).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -I- DOMAIN: DOMAIN VI IS CLOUTIER.
CC -I- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
CC BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
CC BUBBLING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
CC OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
CC NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT
CC MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS
CC BULLOSA.
CC -I- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF GENERALIZED ATROPHIC
CC BENIGN EPIDERMOLYSIS BULLOSA (GABEB). THIS NONLETHAL FORM OF

```
FT DISULFID 293 313 BY SIMILARITY.
FT DISULFID 316 325 BY SIMILARITY.
FT DISULFID 318 343 BY SIMILARITY.
FT DISULFID 346 355 BY SIMILARITY.
FT DISULFID 358 376 BY SIMILARITY.
FT DISULFID 379 392 BY SIMILARITY.
FT DISULFID 381 399 BY SIMILARITY.
FT DISULFID 401 410 BY SIMILARITY.
FT DISULFID 413 428 BY SIMILARITY.
FT DISULFID 431 444 BY SIMILARITY.
FT DISULFID 433 451 BY SIMILARITY.
FT DISULFID 453 462 BY SIMILARITY.
FT DISULFID 465 478 BY SIMILARITY.
FT DISULFID 481 493 BY SIMILARITY.
FT DISULFID 483 500 BY SIMILARITY.
FT DISULFID 502 511 BY SIMILARITY.
FT DISULFID 519 531 BY SIMILARITY.
FT DISULFID 534 546 BY SIMILARITY.
FT DISULFID 536 553 BY SIMILARITY.
FT DISULFID 555 564 BY SIMILARITY.
FT DISULFID 567 578 BY SIMILARITY.
FT DISULFID 581 581 INTERCHAIN (PROBABLE).
FT DISULFID 584 584 INTERCHAIN (PROBABLE).
FT DISULFID 1171 1171 INTERCHAIN (PROBABLE).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 604 604 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 810 810 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 210 210 E -> K (IN CABEE).
FT VARIANT 679 679 /FTID=VAR 004170.
FT CONFLICT 124 124 P -> L (IN JEB).
FT CONFLICT 269 269 /FTID=VAR 004171.
FT CONFLICT 388 388 Q -> R (IN REF. 2).
FT CONFLICT 426 427 MISSING (IN REF. 2).
FT CONFLICT 440 441 P -> A (IN REF. 2).
FT CONFLICT 489 500 QG -> RR (IN REF. 2).
FT CONFLICT 493 500 RD -> E (IN REF. 2).
FT CONFLICT 603 603 LSPQCNQFTGQC -> PQPTVPVHRV (IN REF. 4).
FT CONFLICT 815 815 R -> P (IN REF. 2).
FT CONFLICT 815 815 G -> A (IN REF. 2).

Query Match 8.7%; Score 79.5; DB 1; Length 1172;
Best Local Similarity 25.3%; Pred. No. 6.6;
Matches 41; Conservative 16; Mismatches 66; Indels 39; Gaps 8;

QY 19 ERPPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQRTCAAFCSRSLSC--RKEQG 76
DB 504 EGFGLMCSAAIRQCPRDRTYGDVATG-----CRACDCDFRGTEG 543
QY 77 KFYDHLRLDCISCASICGGQHPKOCAY-FCENKLRSPV-----NLPPELRRQ--RSG 124
DB 544 PGCDKASGRCLCRPGLTGPDCQCGYCN--RYPCVACHPCFTYDADLREQALRFG 600
QY 125 EVENNDSNGRYOGLHRCSEASPALPGKLSDADVALVYST 166
DB 601 RURNATASLWSGFLDRLG-ASRLIDA-KSKIEQTRAVLSS 640

RESULT 14
YL_DROME STANDARD; PRT; 1984 AA.
AC P98163;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative vitellogenin receptor precursor (YL).
GS YL OR YOLKLESS.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Ovary;
RX MEDLINE=951813490; PubMed=7878005;
RA Schonbaum C.P., Lee S., Mahowald A.P.;
RT "The Drosophila yolkless gene encodes a vitellogenin receptor
RT belonging to the low density lipoprotein receptor superfamily.";
RI Proc Natl Acad Sci U S A 92:1485-1489(1995).
CC - FUNCTION INVOLVED IN UPTAKE OF VITELLOGENIN BY ENDOCYTOSIS.
CC - TISSUE SPECIFICITY: OVARY.
CC - SIMILARITY: CONTAINS 13 LDL-RECEPTOR CLASS A DOMAINS.
CC - SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; U13637; AAB60217.1; -.
CC HSSP; P01130; 1AJJ.
CC FlyBase; FBgn004649; Y1.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR002172; LDL_recept A.
CC InterPro; IPR000033; Ldl_receptor_rep.
CC Pfam; PF00008; EGF_5.
CC Pfam; PF00057; ldl_recept_a; 13.
CC Pfam; PF00056; ldl_recept_b; 6.
CC PRINTS; PR00261; LDLRECEPTOR.
CC SMART; SM00179; EGF_CA; 2.
CC SMART; SM00192; EGF_Like; 4.
CC SMART; SM00192; LDLA; 13.
CC SMART; SM00135; LY; 8.
CC PROSITE; PS00010; ASX_HYDROXYL; 2.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS01187; EGF_CA; 2.
CC PROSITE; PS01209; LDLRA_1; 11.
CC PROSITE; PS00068; LDLRA_2; 13.
CC Glycoprotein; Signal; Transmembrane; EGF-like domain; Receptor;
KW Repeat; Endocytosis.
FT SIGNAL 1 ?
FT CHAIN ? 1984 PUTATIVE VITELLOGENIN RECEPTOR.
FT DOMAIN ? 1800 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1801 1821 POTENTIAL.
FT DOMAIN 1822 1984 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 88 126 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 127 167 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 182 222 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 225 264 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 264 306 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 306 347 EGF-LIKE 1. CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 348 388 EGF-LIKE 2.
FT DOMAIN 660 701 EGF-LIKE 3.
FT DOMAIN 984 1026 EGF-LIKE 4.
FT DOMAIN 1029 1064 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 1072 1111 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 1116 1154 LDL-RECEPTOR CLASS A 8.
FT DOMAIN 1156 1195 LDL-RECEPTOR CLASS A 9.
FT DOMAIN 1196 1234 LDL-RECEPTOR CLASS A 10.
FT DOMAIN 1241 1281 LDL-RECEPTOR CLASS A 11.
FT DOMAIN 1281 1320 LDL-RECEPTOR CLASS A 12.
FT DOMAIN 1338 1377 LDL-RECEPTOR CLASS A 13.
FT DOMAIN 1375 1417 EGF-LIKE 5.
FT DOMAIN 1418 1457 EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1734 1770 EGF-LIKE 7.
FT SITE 1837 1878 CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
FT SITE 1878 1892 CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
FT SITE 1892 1902 BY SIMILARITY.
FT DISULFID 90 102 BY SIMILARITY.
FT DISULFID 97 115 BY SIMILARITY.
FT DISULFID 109 124 BY SIMILARITY.
```



```
Query Match      8.6%; Score 78.5; DB 1; Length 630;
Best Local Similarity 23.0%; Pred. No. 4.4;
Matches 38; Conservative 20; Mismatches 54; Indels 53; Gaps 9;

QY 22 POGIWTGVAMRSCPEEQYWDPLLGTCMSCKTICNH-----QSQRTG-----AARCRS--LSGR 72
Db 86 PADVWTPPARASAPSP-----NAQVADHCLKEAAVKICLVCMASPCQEHLOPH 134
QY 73 KEQCKFYDHL-----RDCISCASICGQHPKQCAVFC-----ENKURSPVNL 115
Db 135 FDSPAFDQHPLOPPVRDLL--RRKCSQHNRLREFFCFEHSCEICHCILVEHKTCSPASL- 191
QY 116 PELRRQRSGEVNNSNGRYQGLEHRGSEASPALPGLKLSADQV 160
Db 192 -----SQASADLEAT-----LRHKLTVMYSQINGASRALDDV 223
```

Search completed: January 7, 2003, 09:38:11
Job time : 16.4812 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 47.0125 Seconds
(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-15
Sequence: 1 MSGLSRRSGRSRVDQER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_invertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	15.4	156	Q9N146	Q9n146 macaca mula
2	93	10.2	840	Q96H26	Q96h26 homo sapien
3	93	10.2	1240	O15030	O15030 homo sapien
4	91	10.0	1704	Q94446	Q94446 chironomus
5	89	9.8	839	Q10652	Q10652 caenorhabdi
6	89	9.8	1878	Q9UIF9	Q9uif9 homo sapien
7	88.5	9.7	665	Q9W241	Q9w241 drosophila
8	88.5	9.7	676	Q8SWW8	Q8sww8 drosophila
9	87.5	9.6	415	Q8TCB8	Q8tcb8 homo sapien
10	87	9.6	272	Q9BXV4	Q9bxy4 homo sapien
11	87	9.6	292	Q96K87	Q96k87 homo sapien
12	86.5	9.5	310	Q03108	Q03108 triticum ae
13	86.5	9.5	353	Q03107	Q03107 triticum ae
14	86	9.5	1299	Q26489	Q26489 spodoptera
15	85	9.4	267	Q919M0	Q919m0 neoceratodu
16	85	9.4	1137	Q9H8C1	Q9h8c1 homo sapien

17	85	9.4	1918	4	Q9BOM7	Q9bom7 homo sapien
18	85	9.4	1925	4	Q9P2E3	Q9p2e3 homo sapien
19	84.5	9.3	358	16	Q8ZDV4	Q8zdv4 versinia pe
20	84.5	9.3	598	11	Q8H151	Q8h151 mus musculu
21	84.5	9.3	702	5	Q9VH96	Q9vh96 drosophila
22	83	9.1	820	10	Q9FFK8	Q9ffk8 arabidopsis
23	83	9.1	13288	6	O18758	O18758 sus scrofa
24	82.5	9.1	913	4	Q96EP4	Q96ep4 homo sapien
25	82.5	9.1	1362	13	Q9FVZ4	Q9fvz4 xenopus lae
26	82	9.0	239	13	Q9OZL0	Q9ozl0 fugu rubrip
27	82	9.0	868	5	Q9YIV3	Q9yiv3 polyandroca
28	82	9.0	932	11	Q62030	Q62030 mus musculu
29	82	9.0	1650	11	Q9QVT6	Q9qvt6 rattus sp.
30	81.5	9.0	316	11	Q922H9	Q922h9 mus musculu
31	81	8.9	567	4	Q8WUL3	Q8wul3 homo sapien
32	81	8.9	704	3	O74567	O74567 trichoderma
33	81	8.9	1140	4	Q96KG7	Q96kg7 homo sapien
34	80	8.8	108	16	O07571	O07571 bacillus su
35	80	8.8	330	5	O18118	O18118 caenorhabdi
36	80	8.8	996	11	Q924X6	Q924x6 mus musculu
37	80	8.8	1664	5	Q9TVQ2	Q9tvq2 caenorhabdi
38	80	8.8	1792	13	O57484	O57484 gallus gall
39	79.5	8.7	98	5	O16939	O16939 ancylostoma
40	79.5	8.7	593	10	Q9SEW4	Q9sew4 juglans reg
41	79.5	8.7	1963	5	Q9VY56	Q9vy56 drosophila
42	79.5	8.7	2189	5	Q9B105	Q9b105 eimeria ten
43	79	8.7	217	11	Q9CSB2	Q9csb2 mus musculu
44	79	8.7	269	17	O29751	O29751 archaeoglob
45	79	8.7	317	11	O70524	O70524 cricetus

ALIGNMENTS

RESULT 1
Q9N146 Q9N146 PRELIMINARY; PRT; 156 AA.
ID Q9N146
AC Q9N146;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Transmembrane activator (Fragment).
GN NF-AT.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.
RT "Cytokine Signal Transduction Genes from Rhesus Macaques."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227558; AAF73400.1; -;
FT NON_CODING
SQ SEQUENCE 156 AA; 16170 MW; 8AD74E4D17D511D0 CRC64;

Query Match	15.4%	Score 140; DB 6; Length 156;
Best Local Similarity	96.6%;	Pred. No. 6.1e-08;
Matches 28; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	
Qy 138	GLEHGRSEASPALPGLKLSADQVALVYST 166	
Db 1	GLEHGRSEASPALPGLKLSADQVALVYST 29	
RESULT 2		
ID Q96H26	PRELIMINARY; PRT; 840 AA.	
AC Q96H26;		
DT 01-DEC-2001 (TREMBLrel. 19, Created)		
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)		

```

DE Similar to bromodomain adjacent to zinc finger domain, 2A
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strussberg R;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008965; AAH08965.1; -.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR001965; ZnF_PHD.
DR Pfam; PF02178; AT_hook; 2.
DR Pfam; PF00628; PHD; 1.
DR ProSite; PS50014; BROMODOMAIN_2; 1.
FT NON_TER
SQ
Sequence 840 AA; 94884 MW; 3F8147D9B7034B45 CRC64;

Query Match
Best Local Similarity 10.2%; Score 93; DB 4; Length 840;
Matches 40; Conservative 17; Mismatches 68; Indels 30; Gaps 7;

OY 22 POGMTGVAMRSCEPQWYDPLGTGMSCKTI--CNHQSORTCA-----AFCRSLSCR 72
DB 561 PEGTTEISYEITPRIRVROTLECRSAQVCLCLGQLERSIAMEKSVNKVTC--LVCR 618
OY 73 KEQGFYHLRLDQCISCASICG---QHPKQCA-----YFC-----ENKLRSPVNLPP 116
DB 619 KGDN---DEFLLLCDGCRGCHHYCHRPKMEAVPEGDWFCYCLAQVGEFQKGFPK 675
OY 117 ELRRORSGEVENNSDNGRYOGLERHSGEASPALP 151
DB 676 RGQKKSGYSINFSEGDGRRRVLLRGRESPALP 710

RESULT 3
O15030 PRELIMINARY; PRT; 1240 AA.
AC 015030;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE KIAA0314 protein (Fragment).
GN KIAA0314.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,
RA Tanaka A., Kohari H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 4:114-150(1997).
DR EMBL; AB003112; BAA20773.1; -.
DR HSPF; Q92831; I891.
DR InterPro; IPR000637; AT_hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT_dom.
DR InterPro; IPR001965; ZnF_PHD.
DR Pfam; PF02178; AT_hook; 3.
DR Pfam; PF00439; Bromodomain; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF00628; PHD; 1.
DR PRINTS; PR00929; ATHOOK.

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DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT_hook; 3.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00249; PHD; 1.
DR ProSite; PS50014; BROMODOMAIN_2; 1.
FT NON_TER
SQ
Sequence 1240 AA; 140417 MW; 20BBDFF1A6BGSAL CRC64;

Query Match
Best Local Similarity 10.2%; Score 93; DB 4; Length 1240;
Matches 40; Conservative 17; Mismatches 68; Indels 30; Gaps 7;

OY 22 POGMTGVAMRSCEPQWYDPLGTGMSCKTI--CNHQSORTCA-----AFCRSLSCR 72
DB 961 PEGTTEISYEITPRIRVROTLECRSAQVCLCLGQLERSIAMEKSVNKVTC--LVCR 1018
OY 73 KEQGFYHLRLDQCISCASICG---QHPKQCA-----YFC-----ENKLRSPVNLPP 116
DB 1019 KGDN---DEFLLLCDGCRGCHHYCHRPKMEAVPEGDWFCYCLAQVGEFQKGFPK 1075
OY 117 ELRRORSGEVENNSDNGRYOGLERHSGEASPALP 151
DB 1076 RGQKKSGYSINFSEGDGRRRVLLRGRESPALP 1110

RESULT 4
O94446 PRELIMINARY; PRT; 1704 AA.
AC O94446;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 220 kDa silk protein.
GN SP220.
OS Chironomus thummi (midge).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7154;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Case S.T., Cox C., Bell W.C., Hoffman R.T., Martin J., Hamilton R.;
RT "Extraordinary conservation of cysteines among homologous Chironomus
RT silk proteins sp185 and sp220.";
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U54641; AAA99804.1; -.
DR InterPro; IPR004153; CXCXC_repeat.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000853; McIlhion_nemat.
DR Pfam; PF03128; CXCXC; 69.
DR PRINTS; PR00876; MTNEMATODE.
DR ProSite; PS00022; EGF_1; UNKNOWN_2.
DR ProSite; PS0186; EGF_2; UNKNOWN_1.
SQ
Sequence 1704 AA; 185746 MW; 3A3F20247C8F1E26 CRC64;

Query Match
Best Local Similarity 10.0%; Score 91; DB 5; Length 1704;
Matches 31; Conservative 22; Mismatches 44; Indels 48; Gaps 7;

OY 32 RSCPEQWYD-----FLGTC-----MCKRTCNH-----SQTCAFC 66
DB 1357 QCPNAGQWSDSTCCGCPAAGKCTGAQFMCAGKQCYCPQENCKSPKVPDQTSCTCC 1416
OY 67 -RSLSCRQEQ--GKFTYH-----LRLDQCISCASICGHPKQC---AYF 103
DB 1417 PKNWQPPPGECTAGRTWDATCTEKATVNCESPMWFDATCGCKGCKNKPKLPADRW 1476
OY 104 CENKLRSPVNLPPELRRORSSEVEN 128
DB 1477 CDKCOAVCSLPPITQCPYSGQTVN 1501

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RESULT 5
Q10652 PRELIMINARY; PRT; 839 AA.
ID Q10652;
AC Q10652;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Zinc finger protein CEZF.
GN CEZF.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Rhabditiidae; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RX MEDLINE=96003854; PubMed=7568208;
RA Saha V., Chaplin T., Gregorini A., Ayton P., Young B.D.;
RT "The leukemia-associated-protein (LAP) domain, a cysteine-rich motif,
RT is present in a wide range of proteins, including MLL, AF10, and MLLT6
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9737-9741(1995).
CC -1- SIMILARITY: CONTAINS A CYS-RICH (PHD-FINGER) DOMAIN SIMILAR TO
CC THOSE FROM HAT3.1, MAIZE H0X1A AND PARSLEY PRH.
CR EMBL; U20555; AAC46918.1;
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 2.
KW DNA-binding; Zinc-finger; Metal-binding.
FT DOMAIN 8 54 CYS-RICH (PHD-FINGER).
FT DOMAIN 619 655 LEUCINE ZIPPER.
FT ZN_FING 127 151 POTENTIAL.
FT SEQUENCE 839 AA; 89439 MW; AFBFFB9DD1D3584B8 CRC64;
SQ
Query Match 9.8%; Score 89; DB 5; Length 839;
Best Local Similarity 32.5%; Pred. No. 0.24;
Matches 27; Conservative 8; Mismatches 28; Indels 20; Gaps 5;
QY 34 CPPEQYWDPLLTGCMSC-KTICNHQSQTCAAFRCSLSCRKEQGFYDHLRLDCISCAI 92
Db 130 CNEERENDAKGACMSCKNSKTSRSHVTCQAQ-RKGLLC--BEGAI----- 172
QY 93 CGOHKQCAVFCENKLRSPNLP 115
Db 173 -SRNVKCYG-CENHLKKAINDP 193
RESULT 6
Q9W241 PRELIMINARY; PRT; 1878 AA.
ID Q9W241;
AC Q9W241;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Bromodomain adjacent to zinc finger domain 2A.
GN BAZ2A.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20130112; PubMed=10662543;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes."
RL Genomics 63:40-45(2000).
DR EMBL; AB032254; BAA89211.1; -
DR HSSP; Q92831; 1B91.
DR InterPro; IPR000637; AT_hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT_dom.
DR InterPro; IPR001739; Methy_CpG_bind.
DR InterPro; IPR001965; Znf_PHD.

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DR Pfam; PF02178; AT_hook; 4.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF02731; DDT; 1.
DR Pfam; PF01439; MBD; 1.
DR Pfam; PF00632; PHD; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT_hook; 3.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00391; MBD; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS00104; BROMODOMAIN 2; 1.
SQ SEQUENCE 1878 AA; 208639 MW; 12683AFE636A93A6 CRC64;
Query Match 9.8%; Score 89; DB 4; Length 1878;
Best Local Similarity 23.3%; Pred. No. 0.61;
Matches 37; Conservative 18; Mismatches 66; Indels 38; Gaps 6;
QY 22 PQGLWTGVAMRSPPEEQYWDPLLTGCMSCKTIC-----NHQSQTCAAFRCRS 68
Db 1599 PEGITTEISYEITPRIRIWRQTLQRCSAAHVCLGLHLERSIAWKSVMKVC----- 1652
QY 69 LSCRKEQGFYDHLRLDCISCAICG---QHPKQCA-----YFC-----ENKLRSPV 112
Db 1653 LVCRKGDN---DEFLLCDCGDRGCHVYCHRPKMEAVPEGDWFCVCLCAQQVEGETQKP 1709
QY 113 NLPPELRQRSGEVNNSDNGRYQGLEHRCSEASPALP 151
Db 1710 GFPRGQKRKSGYSLNFSGDRRRRVLLKGRSFAAGP 1748
RESULT 7
Q9W241 PRELIMINARY; PRT; 665 AA.
ID Q9W241;
AC Q9W241;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CG12489 protein.
GN CG12489.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10711132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Y.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Bencos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lin X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R., F. Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,
RA Zhang R.H., Zheng P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2185-2195 (2000).
DR EMBL; AB03457; AAF4688.1; -
DR FlyBase; FBgn0034738; CG12489.
DR InterPro; IPR00299; Band_4.1.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF00373; Band_41; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50057; BAND_41_3; 1.
SQ SEQUENCE 665 AA; 71851 MW; D0281FBA5BA45683 CRC64;

Query Match 9.7%; Score 88.5; DB 5; Length 665;
Best Local Similarity 25.9%; Pred. No. 0.21;
Matches 43; Conservative 19; Mismatches 65; Indels 39; Gaps 9;

DB 2 SGLGRGRGRVDEERFPGQMTGVAMRSCPEQYWDPLTGTCMCKTICNHOSQRT 61
DB 499 TGAGSMAG---KIDLAIREKA-----REAIERCVDTIRISBAMQCK-ICMDRAINT 547
QY 62 CAAFGRSLSCREKQGFYDHLRDCISASICGHPKCAFCENKLRSPVN--LPPELR 119
DB 548 VNPCC---C-----HVIA-CAQCAARCSNCPN-----CRVKITSVVKIYLPPELR 588
QY 120 RORSGEVENNSDNGS-----RYGLEHRSGEASPALPGKLSAD 158
DB 589 TSQTSGATTSSSSIMDQGVBEQLQQQDLDEISAAPASLEAGAD 634

RESULT 8

Q8SWM8 PRELIMINARY; PRT; 676 AA.
AC Q8SWM8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LD18186P.
GN CG12489.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydridae; Drosophilidae; Drosophila.
OX NCB1_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne W., Chavez C., Dorsett V., Dresnek D., Fartin D., Frise E.,
RA George R., Gonzalez M., Guatin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Pargass V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY095033; AAM1360.1; -
SQ SEQUENCE 676 AA; 73182 MW; 8359E26A02CCDC87 CRC64;

Query Match 9.7%; Score 88.5; DB 5; Length 676;
Best Local Similarity 25.9%; Pred. No. 0.22;
Matches 43; Conservative 19; Mismatches 65; Indels 39; Gaps 9;
QY 2 SGLGRGRGRVDEERFPGQMTGVAMRSCPEQYWDPLTGTCMCKTICNHOSQRT 61
DB 510 TGAGSMAG---KIDLAIREKA-----REAIERCVDTIRISBAMQCK-ICMDRAINT 558
QY 62 CAAFGRSLSCREKQGFYDHLRDCISASICGHPKCAFCENKLRSPVN--LPPELR 119
DB 559 VNPCC---C-----HVIA-CAQCAARCSNCPN-----CRVKITSVVKIYLPPELR 599
QY 120 RORSGEVENNSDNGS-----RYGLEHRSGEASPALPGKLSAD 158
DB 600 TSQTSGATTSSSSIMDQGVBEQLQQQDLDEISAAPASLEAGAD 645

DB 510 TGAGSMAG---KIDLAIREKA-----REAIERCVDTIRISBAMQCK-ICMDRAINT 558
QY 62 CAAFGRSLSCREKQGFYDHLRDCISASICGHPKCAFCENKLRSPVN--LPPELR 119
DB 559 VNPCC---C-----HVIA-CAQCAARCSNCPN-----CRVKITSVVKIYLPPELR 599
QY 120 RORSGEVENNSDNGS-----RYGLEHRSGEASPALPGKLSAD 158
DB 600 TSQTSGATTSSSSIMDQGVBEQLQQQDLDEISAAPASLEAGAD 645

RESULT 9

Q8TCB8 PRELIMINARY; PRT; 415 AA.
AC Q8TCB8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 45.2 kDa protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022399; AAH2399.1; -
KW Hypothetical protein.
FT HYPOTHEMETICAL PROTEIN.
SQ SEQUENCE 415 AA; 45230 MW; 945069C1607D38E3 CRC64;

Query Match 9.6%; Score 87.5; DB 4; Length 415;
Best Local Similarity 23.8%; Pred. No. 0.16; 71; Indels 51; Gaps 11;
Matches 46; Conservative 25; Mismatches 71; Indels 51; Gaps 11;

QY 6 RSRGRGRVDEERF---PQGLTGVAMRSC-PBEQYWDPLTGTCMCKTICNHOSQ-- 59
DB 89 RGRRG-----ENLFAITDGMVPLAMEHHEHREHYNLSAATC-SFGMCCHYTGV 140
QY 60 --RTCAAFGRSLSCREKQGFYDHLRDCIS-----ASICGHP-----KCC-AYF 103
DB 141 WAKTIRICGSHFCFKLQGVETNI--ELVCNVEPPGNVAKRPPYDGTFCSCQCPGYN 198
QY 104 CENKLRSPVNLP-----PELRORSGEVENNSDNGRYOGL-----EHRGS 144
DB 199 CKNSLCEPIGSPEDQODPLVLTAPSPRATASDSRMGTSPSIATGI PAFVLTVEVGS 258
QY 145 EASPALPGKLSA 157
DB 259 LATKALPAVEVQA 271

RESULT 10

Q9BXV4 PRELIMINARY; PRT; 272 AA.
AC Q9BXV4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Thrombospondin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MAO Y., Xie Y., Zhao Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,
RA Tang R., Chen X., Wu C.;
RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.

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RC TISSUE=PLACENTA;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251057; AAK34947.1; -
DR EMBL; BC022367; AAH22367.1; -
DR InterPro; IPR002174; Fusin-like.
DR InterPro; IPR000884; TSF1.
DR Pfam; PF00090; tsf_1; 1.
DR SMART; SM00261; TSF; 2.
DR SMART; SM00209; TSF1; 1.
DR PROSITE; PS50092; TSF1; 1.
SQ SEQUENCE 272 AA; 30928 MW; CACAEC6B7E781189 CRC64;

Query Match
Best Local Similarity 24.6%; Score 87; DB 4; Length 292;
Matches 42; Conservative 18; Mismatches 59; Indels 52; Gaps 11;

QY 28 GVAMRSCPEQYWD--PLLGTCMSCKTICNHOSQRTCAAFCSRSLKQKGFYDHL---- 82
DB 74 GVCLLSCPSSGYGTRYDPIKCTCKKADCD----TC--FNKNF-CTKCKSGFYHLGKRC 125
QY 83 LRDC-----ISCASI-----CGQHPKQCA--FCENKLRSPV----- 112
DB 126 LONCPGLEANNHTMECVSIHVCSEWNPSPCTKKGKTCGKRGTTVRREIIQHPSA 185
QY 113 --NLPPRLRQRSGEVNNSDNGR--YQGLEHR-----GSEASPALPGLK 154
DB 186 KGNLCPTNETRKTCTVQKCKQGERKKRKRKPKNGKESKEAIPDSK 236

RESULT 11
Q96K87 PRELIMINARY; PRT; 292 AA.
AC Q96K87;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDNA FJ14440 f1s, Clone HEMBB100915, weakly similar to
DE subtilisin-like protease PACE4 precursor (EC 3.4.21.-).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=EMBRYO;
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.,
RA "NEO human cDNA sequencing project",
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027346; BAB55051.1; -
DR InterPro; IPR000861; EGF-like.
DR InterPro; IPR000864; TSF1.
DR Pfam; PF00090; tsf_1; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50092; TSF1; 1.
SQ SEQUENCE 292 AA; 33243 MW; 01E2774AC3D4A6F8 CRC64;

Query Match
Best Local Similarity 24.6%; Score 87; DB 4; Length 292;
Matches 42; Conservative 18; Mismatches 59; Indels 52; Gaps 11;

QY 28 GVAMRSCPEQYWD--PLLGTCMSCKTICNHOSQRTCAAFCSRSLKQKGFYDHL---- 82
DB 74 GVCLLSCPSSGYGTRYDPIKCTCKKADCD----TC--FNKNF-CTKCKSGFYHLGKRC 125
QY 83 LRDC-----ISCASI-----CGQHPKQCA--FCENKLRSPV----- 112
DB 126 LONCPGLEANNHTMECVSIHVCSEWNPSPCTKKGKTCGKRGTTVRREIIQHPSA 185
QY 113 --NLPPRLRQRSGEVNNSDNGR--YQGLEHR-----GSEASPALPGLK 154
DB 186 KGNLCPTNETRKTCTVQKCKQGERKKRKRKPKNGKESKEAIPDSK 236

RESULT 12
Q03108 PRELIMINARY; PRT; 310 AA.
AC Q03108;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cathepsin B (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=VAR. CHINESE SPRING;
RX MEDLINE=93258430; PubMed=1302642;
RA Cejudo F.J., Murphy G., Chinoy C., Baulcombe D.C.;
RA "A gibberellin-regulated gene from wheat with sequence homology to
RT cathepsin B of mammalian cells.";
RL Plant J. 2:937-948 (1992).
DR EMBL; X66014; CAA46812.1; -
DR HSSP; P07688; 1QDQ.
DR MEROPS; C01.049.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000189; SHprot_scsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR PRODOM; PD000158; Peptidase_C1; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
DR Hydrolase; Thiol protease.
KT NON TER 310 310
SQ SEQUENCE 310 AA; 33811 MW; 2DE6F3264BB228C3 CRC64;

Query Match
Best Local Similarity 24.7%; Pred. No. 0.15;
Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;

QY 22 PQGLWTGVAMRSCPE-----EQYWDPLLGTCMSCKTICNHOSQRTCAAFCSRSLSCR 72
DB 80 PPGLLAGVPIKIHPMDLPKEFDARTQWS-----SCSTIGNILDQHCACWAFAAVE 132
QY 73 KEQKGFYDHL-----LRDCISCAICGQHPKQCAVFCENKLRSPVNLPPELRRQRSGE 125
DB 133 ALQDRFCIHLNMSVSLSVNDLLAC-----CGFLCGSGCGGYPISAWRYFRSGV 182
QY 126 VENNSDNGRYQGLEHRGSEASPALP 151
DB 183 VTEECDPYFDOTGQHPGCE--PAYP 206

RESULT 13
Q03107 PRELIMINARY; PRT; 353 AA.
AC Q03107;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cathepsin B (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=VAR. CHINESE SPRING;

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RX MEDLINE=93258430; PubMed=1302642;
 RA Celjudo F.J., Murphy G., Chiny C., Baulcombe D.C.;
 RT "A gibberellin-regulated gene from wheat with sequence homology to
 RT cathepsin B of mammalian cells.";
 RL Plant J. 2:937-948 (1992).
 DR EMBL: X66013; CAA46811.1; -
 DR HSRP; P07688; I0Q0.
 DR MEROPS: C01.649.
 DR InterPro; IPR001668; Peptidase_C1.
 DR InterPro; IPR001691; SH3PROT_acite.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPAIN.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
 KW Hydrolase; Thiol protease.
 FT NON_TER
 SQ SEQUENCE 353 AA; 38355 MW; A10E7C84ED46EA44 CRC64;

Query Match 9.5%; Score 86.5; DB 10; Length 353;
 Best Local Similarity 24.7%; Pred. No. 0.18;
 Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;
 OY 22 PGLMTGVAMRSCEP-----EGYWPDLTGTCMSCKTICNHQSQRCAAFCRSLSGR 72
 DB 80 PGLLAGVPIKIHPEMDLPKEPDPARTQWS-----SCSTIGNILDQHGCAWPAVAVE 132
 OY 73 KGGKRYDHL-----LRDCTSCASICGQHPKQCAVFCENKLRSPVNLPELRRQSGE 125
 DB 133 ALQDRFCILHMSVSLSVNDLLAC-----CGFLGSGCNGGYPISAMRYPRRSQV 182
 OY 126 VERNSSNGRYOGLERHSGEASAPALP 151
 DB 183 VTBECDPYDQTCQHPCCE--PAYP 206

RESULT 14
 OQ6489 PRELIMINARY; PRT; 1299 AA.
 AC OQ6489;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoprotease furin.
 GN Spodoptera frugiperda (Fall armyworm).
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Noctuidae; Amphipylinae; Spodoptera.
 OX NCBI_TaxID=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SF9;
 RA Cieplik M., Klenk H.;
 RT "Cloning and functional characterization of FURIN from Spodoptera
 RT frugiperda (SF9) cells.";
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z68868; CAA3116.1; -
 DR HSRP; Q99405; IMPT.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002029; Peptidase_S8.
 DR Pfam; PF01483; P; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Protease.
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;

Query Match 9.5%; Score 86; DB 5; Length 1299;
 Best Local Similarity 25.0%; Pred. No. 0.87;
 Matches 39; Conservative 16; Mismatches 51; Indels 50; Gaps 9;
 OY 22 PGLMTGVAMRSCEPEQYWPDLTGTCMSCKTICNHQSQRCAAFCRSLSCKEGKF--- 78
 DB 1104 PRFMDGGLCMEGLSGQYVDATSGTCRSDASC-----RTSG-----EGFSCT 1148
 OY 79 -----YDHLRDCISASICG---QHPRQCAVFCENKLRSPVNLPELRRQSGEVE 127
 DB 1149 TCSRRLRIDRLANQVPPCCSERGVNTSPYDCCG-CN-----PE-----NGSCT 1192
 OY 128 NNSDNGRYOGLERHSGEASAPALPGLKLSADQVALY 163
 DB 1193 NSS-VAGKRRIAEWGLHTAPSD---AAPSVAIV 1223

RESULT 15
 OQ19M0 PRELIMINARY; PRT; 267 AA.
 AC OQ19M0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Proenkephalin.
 OS Neoceratodus forsteri (Australian lungfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
 OX NCBI_TaxID=7892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRNIN.
 RA MEDLINE=20417836; PubMed=10960597;
 RA Sollars C., Danielson P., Joss U.M.P., Dore R.M.;
 RT "Deciphering the origin of Met-enkephalin and Leu-enkephalin in Lobe-
 RT fished fish: cloning of Australian lungfish proenkephalin.";
 RL Brain Res. 874:131-136 (2000).
 DR EMBL; AF232671; AAF44658.1; -
 DR InterPro; IPR000094; Opioid_neuropep.
 DR Pfam; PF01160; Opioid_neuropep; 1.
 DR PRINTS; PR01028; OPIOIDPRCKSR.
 DR PROSITE; PS01252; OPIOIDS_PRECURSOR; UNKNOWN 1.
 SQ SEQUENCE 267 AA; 30688 MW; 69C92C0F378E0F0 CRC64;

Query Match 9.4%; Score 85; DB 13; Length 267;
 Best Local Similarity 29.4%; Pred. No. 0.19;
 Matches 30; Conservative 7; Mismatches 35; Indels 30; Gaps 5;
 OY 62 CAAFCRSLSCKEGKFYDHLRDCISASICGQH---PQCAVFCENKLRSPVNSWDMC 110
 DB 15 CA--CLILAVAECK-----DCAHTYHGLGADINPLSTLCEGCKLPVSRWDMC 65
 OY 111 ----PVNLPELRRQSGEVENNSDN-----SGRYOGLERH 142
 DB 66 KELLYGKPEIMQBEETIASVENDKENDQRMFAKRYGFMGR 107

Search completed: January 7, 2003, 09:40:10
 Job time : 50.0125 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:14 ; Search time 20.386 seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-15
Perfect score: 909
Sequence: 1 MSGIGRRGRGSRVDQBER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pdp.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	166	2	US-08-810-572A-6
2	909	100.0	166	4	US-09-290-333-6
3	909	100.0	293	2	US-08-810-572A-2
4	909	100.0	293	4	US-09-290-333-2
5	82.5	9.1	799	2	US-08-525-940-23
6	82.5	9.1	799	2	US-08-976-838-23
7	82.5	9.1	881	2	US-08-525-940-21
8	82.5	9.1	881	2	US-08-976-838-21
9	82.5	9.1	915	2	US-08-525-940-18
10	82.5	9.1	915	2	US-08-976-838-18
11	82.5	9.1	915	4	US-09-214-555B-2
12	82.5	9.1	915	4	US-09-214-555B-7
13	81	8.9	704	4	US-09-590-656-2
14	81	8.9	977	4	US-09-590-656-1
15	81	8.9	1124	1	US-08-323-474-2
16	81	8.9	1124	5	PCT-US93-06093-2
17	79.5	8.7	98	2	US-08-465-380-21
18	79.5	8.7	98	2	US-08-480-478-49
19	79.5	8.7	98	2	US-08-486-397-21
20	79.5	8.7	98	2	US-08-486-392-21
21	79.5	8.7	98	2	US-08-461-965-21
22	79.5	8.7	98	2	US-08-326-110A-49
23	79.5	8.7	98	2	US-08-634-641-21
24	79.5	8.7	98	3	US-09-249-471-21
25	79.5	8.7	98	3	US-09-249-472-21
26	79.5	8.7	98	3	US-09-249-451-21
27	79.5	8.7	98	3	US-08-809-455-21

28	79.5	8.7	98	3	US-09-249-461-21	Sequence 21, Appl
29	79.5	8.7	98	3	US-09-249-448-21	Sequence 21, Appl
30	77.5	8.6	518	1	US-08-385-229-4	Sequence 4, Appl
31	77.5	8.5	75	2	US-08-465-380-6	Sequence 6, Appl
32	77.5	8.5	75	2	US-08-465-380-41	Sequence 41, Appl
33	77.5	8.5	75	2	US-08-480-478-35	Sequence 35, Appl
34	77.5	8.5	75	2	US-08-486-397-6	Sequence 6, Appl
35	77.5	8.5	75	2	US-08-486-397-41	Sequence 41, Appl
36	77.5	8.5	75	2	US-08-486-399-6	Sequence 6, Appl
37	77.5	8.5	75	2	US-08-486-399-41	Sequence 41, Appl
38	77.5	8.5	75	2	US-08-461-965-6	Sequence 6, Appl
39	77.5	8.5	75	2	US-08-461-965-41	Sequence 41, Appl
40	77.5	8.5	75	2	US-08-326-110A-35	Sequence 35, Appl
41	77.5	8.5	75	2	US-08-634-641-6	Sequence 6, Appl
42	77.5	8.5	75	2	US-08-634-641-41	Sequence 41, Appl
43	77.5	8.5	75	3	US-09-249-471-6	Sequence 6, Appl
44	77.5	8.5	75	3	US-09-249-471-41	Sequence 41, Appl
45	77.5	8.5	75	3	US-09-249-472-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-6

Query Match 100.0%; Score 909; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-90;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERPPGGLMTGVMARSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERPPGGLMTGVMARSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60

QY 61 TCAAFGRSLSCRKEGKGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFGRSLSCRKEGKGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166

RESULT 2
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 100.0%; Score 909; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERPPGGLMTGVMARSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERPPGGLMTGVMARSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60

QY 61 TCAAFGRSLSCRKEGKGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120

DB 61 TCAAFGRSLSCRKEGKGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166

RESULT 3
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-2

Query Match 100.0%; Score 909; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERPPGGLMTGVMARSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERPPGGLMTGVMARSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60

QY 61 TCAAFGRSLSCRKEGKGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFGRSLSCRKEGKGFYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166

RESULT 4
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match 100.0%; Score 909; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 TCAAFRCRSLSCRKEQKQFYDHLRDCISCAICGQHPKQCAFCENKLRSPVNLPELRR 120
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DB 121 QRSGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
RESULT 5
US-08-525-940-23
; Sequence 23, Application US/08525940
; Patent No. 5866351
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; APPLICANT: Miranda, Luis R.

APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-23
Query Match 9.1%; Score 82.5; DB 2; Length 799;
Best Local Similarity 26.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEQYWDPLLTGTCMCKTICNHQSOR TCAAF-----CR-----SLSG 71
DB 603 TNSCVTHCPDGSYQDTKKNLCRKSENC-----KTCTEFHNTCTCRDGLSLGSRCSVSC 657
QY 72 RKEQKQFYDHLRDCISCAIC-----GQHPKQ-----AYECEN 106
DB 658 --EDGRVFNQ--QDCQCHRPATCAGAGADGCINCTEGYFMD 697
RESULT 6
US-08-976-838-23
; Sequence 23, Application US/08976838
; Patent No. 5981259
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
; MOLECULES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/976,838
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-23

Query Match 9.1%; Score 82.5; DB 2; Length 799;
Best Local Similarity 26.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYWDPLGTCTMCKTICNHOSORTCAAF-----CR-----SLSC 71
Db 603 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTECRDGLSLQSRCSVSC 657
Qy 72 RKEQKFFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 658 --EDGRYFNG--QDCQPCRFCAATCAGAGADGCTNCTEGTFMED 697

RESULT 7
US-08-525-940-21
Sequence 21, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYWDPLGTCTMCKTICNHOSORTCAAF-----CR-----SLSC 71
Db 665 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTECRDGLSLQSRCSVSC 739
Qy 72 RKEQKFFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCQPCRFCAATCAGAGADGCTNCTEGTFMED 779

RESULT 8
US-08-976-838-21
Sequence 21, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYWDPLGTCTMCKTICNHOSORTCAAF-----CR-----SLSC 71
Db 665 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTECRDGLSLQSRCSVSC 739
Qy 72 RKEQKFFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCQPCRFCAATCAGAGADGCTNCTEGTFMED 779

us-09-855-158-15-rai

Tue Jan 7 10:36:49 2003

ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/976,838
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-18

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773
QY 72 RKEQGFYDHLRLDCISCAIC---GQHPKQC-----AYFCEN 106
DB 774 --EDGRYFNG--QDQPCHRFCATCAGAGADGCTGCTGYFMED 813

RESULT 11
US-09-214-555B-2
Sequence 2, Application US/09214555B
Patent No. 6380171
GENERAL INFORMATION:
APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILE REFERENCE: PRO-PROTEIN CONVERT ENZ
CURRENT APPLICATION NUMBER: US/09/214,555B
PRIOR FILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: 60/021,008
PRIOR FILING DATE: 1996-07-26
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR FILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-555B-2

Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773

RESULT 10
US-08-976-838-18
Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-18

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773
QY 72 RKEQGFYDHLRLDCISCAIC---GQHPKQC-----AYFCEN 106
DB 774 --EDGRYFNG--QDQPCHRFCATCAGAGADGCTGCTGYFMED 813

RESULT 10
US-08-525-940-18
Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/976,838
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-18

Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773
QY 72 RKEQGFYDHLRLDCISCAIC---GQHPKQC-----AYFCEN 106
DB 774 --EDGRYFNG--QDQPCHRFCATCAGAGADGCTGCTGYFMED 813

RESULT 10
US-08-525-940-18
Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

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us-09-855-158-15.rat

Page 6

QY 72 RKEQKFEYDHLRDCISASIC-----GQHEKQC-----AYPCEN 106
DB 774 -EDGRYFNG--ODCOPCHRCATCAGAGADGCTGCTEGYFMD 813

RESULT 12

US-09-214-555B-7
; Sequence 7, Application US/09214555B
; Patent No. 6380171
; GENERAL INFORMATION:
; APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTREAL
; TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
; FILE REFERENCE: PRO-PROTEIN CONVERT ENZ
; CURRENT APPLICATION NUMBER: US/09/214,555B
; PRIORITY FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: 60/021,008
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: 2,203,745
; PRIOR FILING DATE: 1997-04-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-555B-7

Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8; Mismatches 34; Indels 33; Gaps 7;
Matches 27; Conservative 10;

QY 27 TGVMASCEPEOYWDPLGTGCMCKTICNHSORTCAAF-----CR-----SISC 71
DB 719 TNSVTHCPGOSTYDTKNCCKKSCNC-----KCTEPHNCCECHDGLSLOGSCRSVSC 773
QY 72 RKEQKFEYDHLRDCISASIC-----GQHEKQC-----AYPCEN 106
DB 774 -EDGRYFNG--ODCOPCHRCATCAGAGADGCTGCTEGYFMD 813

RESULT 13

US-09-590-656-2
; Sequence 2, Application US/09590656
; Patent No. 641932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, Iii, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-2

Query Match 8.9%; Score 81; DB 4; Length 704;
Best Local Similarity 24.2%; Pred. No. 1.8; Mismatches 63; Indels 44; Gaps 8;
Matches 39; Conservative 15;

QY 26 WTGVAMSCPEOYWD-----LLGTGM-----SCKTICN-HSQ 59
DB 203 FTFLIVARC-EAQKMBECHNLCTACNNNGVCHEDGECICPPGMRCTCEKACELHTFG 261
QY 60 RTCAAFGRSLSCREKQKFTYDHLRDCISASICGQHPKQCAVFCENKLRSPVNLPELR 119
DB 262 RTCKERCSCG---QEGKSYVFCFLPDYGCSCATGKGLQCNBACH-----PGFYGPCK 312

QY 120 RQSGEVENNSDNGRYGGLERHGSASPALPGLKLSADOV 160
DB 313 LRCSG---NNGEMCDRFQ-----GCLCSPGMOGLQCEREGI 345

RESULT 14

US-09-590-656-1
; Sequence 1, Application US/09590656
; Patent No. 641932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, Iii, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-1

Query Match 8.9%; Score 81; DB 4; Length 977;
Best Local Similarity 24.2%; Pred. No. 2.8; Mismatches 63; Indels 44; Gaps 8;
Matches 39; Conservative 15;

QY 26 WTGVAMSCPEOYWD-----LLGTGM-----SCKTICN-HSQ 59
DB 203 FTFLIVARC-EAQKMBECHNLCTACNNNGVCHEDGECICPPGMRCTCEKACELHTFG 261
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DB 262 RTCKERCSCG---QEGKSYVFCFLPDYGCSCATGKGLQCNBACH-----PGFYGPCK 312
QY 120 RQSGEVENNSDNGRYGGLERHGSASPALPGLKLSADOV 160
DB 313 LRCSG---NNGEMCDRFQ-----GCLCSPGMOGLQCEREGI 345

RESULT 15

US-08-323-474-2
; Sequence 2, Application US/08323474
; Patent No. 5447860
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,474
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-474-2

Query Match 8.9%; Score 81; DB 1; Length 1124;
Best Local Similarity 24.2%; Pred. No. 3.3;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;
QY 26 WTGVAMRSCPBEQYWDP-----LLGTCM-----SCKTICN-HQSQ 59
DB 203 FTFLIVVRC-EAQKVGPECNHLCTACMNGVCHDTGECICPPGFMGRCTCEKACELHTEG 261
QY 60 RTCAAFCSLSCKEQGKFYDHLRLDCISCASTCGQHPKQCAVFCENKLRSPVNLPPPELR 119
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QY 120 RORSGEVNNSDNSGRYQGLEHRRGSEAPALPGLKLSADOV 160
DB 313 LRCSC---NNGEMCDRFQ-----GCLCSFGWQGLQCEREGI 345

Search completed: January 7, 2003, 09:42:07
Job time : 22.386 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:40:20 ; Search time 12.4812 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-15

Perfect score: 909

Sequence: 1 MSGLGRSRGGRSRVDQER.....SPALFGLKLSADQVALVYST 166

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Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	909	100.0	293	9	US-09-779-050A-42
3	909	100.0	293	9	US-10-084-971-2
4	909	100.0	293	10	US-09-879-919-22
5	909	100.0	293	10	US-09-854-864-14
6	909	100.0	293	10	US-09-961-376-2
7	904	99.4	293	10	US-09-854-864-18
8	894.5	98.4	291	9	US-09-779-050A-43
9	393	43.2	67	10	US-09-854-864-16
10	342	37.6	59	10	US-09-854-864-20
11	279.5	30.7	57	9	US-09-779-050A-47
12	224	24.6	38	9	US-09-779-050A-46
13	218	24.0	37	9	US-09-779-050A-45
14	168	18.5	32	9	US-09-779-050A-44
15	93	10.2	81	10	US-09-854-864-13
16	87.5	9.6	463	9	US-09-905-291A-285
17	87.5	9.6	463	9	US-09-902-853-285
18	87.5	9.6	463	9	US-09-907-824-285
19	87.5	9.6	463	9	US-09-907-841-285

20	87.5	9.6	463	10	US-09-909-320-285	Sequence 285, App
21	87.5	9.6	463	10	US-09-909-088B-285	Sequence 285, App
22	87	9.6	207	9	US-10-077-438-3	Sequence 3, Appli
23	87	9.6	207	9	US-10-077-437-3	Sequence 3, Appli
24	87	9.6	292	10	US-09-745-763-166	Sequence 166, App
25	86	9.5	231	10	US-09-840-795-19	Sequence 19, Appl
26	86	9.5	299	9	US-10-119-466-12	Sequence 12, Appl
27	84	9.2	77	10	US-09-840-795-17	Sequence 17, Appl
28	79.5	8.7	1172	9	US-09-974-398-56	Sequence 56, Appl
29	79.5	8.7	1172	10	US-09-919-172-16	Sequence 16, Appl
30	78.5	8.6	399	10	US-09-907-372-1	Sequence 1, Appli
31	77.5	8.5	220	9	US-10-042-141-54	Sequence 54, Appl
32	77.5	8.5	220	10	US-09-726-643-54	Sequence 54, Appl
33	77.5	8.5	514	10	US-09-800-729-124	Sequence 124, App
34	77.5	8.5	1745	10	US-09-800-729-89	Sequence 89, Appl
35	77.5	8.5	1762	9	US-10-044-807-2	Sequence 2, Appli
36	77.5	8.5	1766	10	US-09-764-853-554	Sequence 554, App
37	77	8.5	1184	9	US-09-992-598-124	Sequence 124, App
38	77	8.5	1184	9	US-09-989-293A-124	Sequence 124, App
39	77	8.5	1184	9	US-09-989-735-124	Sequence 124, App
40	77	8.5	1184	9	US-09-990-444-124	Sequence 124, App
41	77	8.5	1184	9	US-09-989-730-124	Sequence 124, App
42	77	8.5	1184	9	US-09-990-436-124	Sequence 124, App
43	77	8.5	1184	9	US-09-991-181-124	Sequence 124, App
44	77	8.5	1184	9	US-09-993-687-124	Sequence 124, App
45	77	8.5	1184	10	US-09-757-716-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-854-864-15

; Sequence 15, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854.864

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 15

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-15

Query Match 100.0%; Score 909; DB 10; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.6e-75;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRSRGGRSRVDQERFPQGLWTGVMRSCPEEQYWDPLLTCTMCKTICNHSQR 60

Db 1 MSGLGRSRGGRSRVDQERFPQGLWTGVMRSCPEEQYWDPLLTCTMCKTICNHSQR 60

QY 61 TCAAFCSLSCKRQKGFYDHLRDCISASCISGQHPQCAVFCENKLSRSPVNLPELRR 120

Db 61 TCAAFCSLSCKRQKGFYDHLRDCISASCISGQHPQCAVFCENKLSRSPVNLPELRR 120

QY 121 QRSGEVNNNSNGRYQGLEHRSSEASPALGLKLSADQVALVYST 166

Db 121 QRSGEVNNNSNGRYQGLEHRSSEASPALGLKLSADQVALVYST 166

RESULT 2

US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-5708
; CURRENT FILING DATE: 2001-02-12
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRDCISGASICGHPKOCAYFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRDCISGASICGHPKOCAYFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLGHRGSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLGHRGSEASPALPGIKLSADQVALVYST 166

RESULT 3
US-10-084-971-2
; Sequence 2, Application US/10084971
; Publication No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin- α Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/533,822
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-971-2

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRDCISGASICGHPKOCAYFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRDCISGASICGHPKOCAYFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVNNSDNSGRYQGLGHRGSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLGHRGSEASPALPGIKLSADQVALVYST 166

RESULT 4
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: YU, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253PI
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US/09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGSRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRDCISGASICGHPKOCAYFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRDCISGASICGHPKOCAYFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLGHRGSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLGHRGSEASPALPGIKLSADQVALVYST 166

RESULT 5
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match          100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
QY 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166

RESULT 6
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor Tr17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961.376
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match          100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
QY 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166

RESULT 7
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-866B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match          99.4%; Score 904; DB 10; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.2e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
QY 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVALVYS 165
DB 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVALVYS 165

RESULT 8
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match          98.4%; Score 894.5; DB 9; Length 291;
Best Local Similarity 99.4%; Pred. No. 6e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCTMCKTICNHQSQR 60
QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAAYFCENKLRSPVNLPPELRR 120
QY 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVENNSDNGRYQGLEHRRGSEASPALPGLKLSADQVA-VYST 165

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Tue Jan 7 10:36:49 2003

us-09-855-158-15.rapb

Page 4

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RESULT 9
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match
Best Local Similarity 94.4%; Score 393; DB 10; Length 67;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 34 CPEQYWDPLGTGCMCKTICNHSQRTCAFRSLSCREKQKFDHLRDCISGASIC 93
Db 1 CPEQYWDPLGTGCMCKTICNHSQRTCAFC---CRKQKFDHLRDCISGASIC 56

Qy 94 GQHPKOCAYFC 104
Db 57 GQHPKOCAYFC 67

RESULT 10
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match
Best Local Similarity 100.0%; Score 342; DB 10; Length 59;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 CPEQYWDPLGTGCMCKTICNHSQRTCAFRSLSCREKQKFDHLRDCISGASIC 92
Db 1 CPEQYWDPLGTGCMCKTICNHSQRTCAFRSLSCREKQKFDHLRDCISGASIC 59

RESULT 11
US-09-779-050A-47
; Sequence 47, Application US/09779050A
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; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 47
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-47

Query Match
Best Local Similarity 98.3%; Score 279.5; DB 9; Length 57;
Matches 57; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 108 LRSFVNLPELRORSGEVENSNDNGRYQGLHHRGSEASPALPKLSADQVALVYS 165
Db 1 LRSFVNLPELRORSGEVENSNDNGRYQGLHHRGSEASPALPKLSADQVA-VYS 57

RESULT 12
US-09-779-050A-46
; Sequence 46, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 46
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-46

Query Match
Best Local Similarity 100.0%; Score 224; DB 9; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 SCRKQKQKFDHLRDCISGASICGQHPKOCAYFCENK 107
Db 1 SCRKQKQKFDHLRDCISGASICGQHPKOCAYFCENK 38

RESULT 13
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 45
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 278.331 Seconds
(without alignments)
384.527 Million cell updates/sec

Title: US-09-855-158-15

Perfect score: 909

Sequence: 1 MSGLSRRGRSRVDQBER.....SPALFGLKLSADQVALVYST 166

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	909	100.0	166	21	US-09-782-857-6
3	909	100.0	166	21	US-09-782-857A-6
4	909	100.0	166	22	US-09-854-864-15
5	909	100.0	166	22	US-09-855-158-15
6	909	100.0	265	21	US-09-724-341-9

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7 909 100.0 293 1 PCT-US00-07966-2 Sequence 2, Appli
8 909 100.0 293 1 PCT-US01-19026-2 Sequence 2, Appli
9 909 100.0 293 1 PCT-US02-1618-6 Sequence 4, Appli
10 909 100.0 293 12 US-08-810-572-6 Sequence 2, Appli
11 909 100.0 293 17 US-09-302-863-2 Sequence 6, Appli
12 909 100.0 293 18 US-09-479-856-6 Sequence 2, Appli
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32 904 99.4 397 22 US-09-855-158-18 Sequence 18, Appli
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35 890 97.9 245 19 US-09-569-245-9 Sequence 9, Appli
36 890 97.9 245 20 US-09-627-206-9 Sequence 9, Appli
37 700 77.0 392 25 US-10-152-363A-50 Sequence 50, Appli
38 599 65.9 120 18 US-09-479-856-4 Sequence 4, Appli
39 599 65.9 120 19 US-09-569-245-4 Sequence 4, Appli
40 599 65.9 120 20 US-09-627-206-4 Sequence 4, Appli
41 599 65.9 247 18 US-09-479-856-2 Sequence 2, Appli
42 599 65.9 247 19 US-09-569-245-2 Sequence 2, Appli
43 599 65.9 247 20 US-09-627-206-2 Sequence 2, Appli
44 525 57.8 357 25 US-10-152-363A-56 Sequence 56, Appli
45 469 51.6 332 25 US-10-152-363A-62 Sequence 62, Appli

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ALIGNMENTS

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RESULT 1
US-08-810-572-6
; Sequence 6, Application US/08810572
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

```

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572-6

Query Match 100.0%; Score 909; DB 12; Length 166;
Best Local Similarity 100.0%; Pred. No. 1,4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSGLSRRGGRSRVDOERFPOGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSQR 60
DB 1 MSGLSRRGGRSRVDOERFPOGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSQR 60
OY 61 TCAAFCRSLSCRKQKGFYDHLRDICSCASICGQHPKQCAFECNKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKQKGFYDHLRDICSCASICGQHPKQCAFECNKLRSPVNLPEELRR 120
OY 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166

RESULT 2
US-09-782-857-6
Sequence 6, Application US/09782857
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857-6

Query Match 100.0%; Score 909; DB 21; Length 166;
Best Local Similarity 100.0%; Pred. No. 1,4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSGLSRRGGRSRVDOERFPOGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSQR 60
DB 1 MSGLSRRGGRSRVDOERFPOGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSQR 60
OY 61 TCAAFCRSLSCRKQKGFYDHLRDICSCASICGQHPKQCAFECNKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKQKGFYDHLRDICSCASICGQHPKQCAFECNKLRSPVNLPEELRR 120
OY 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166

RESULT 3
US-09-782-857A-6
Sequence 6, Application US/09782857A
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear

```
MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match      100.0%; Score 909; DB 21; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 4
US-09-854-864-15
; SEQUENCE 15, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-866B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match      100.0%; Score 909; DB 22; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 5
US-09-855-158-15
; SEQUENCE 15, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-866B
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      100.0%; Score 909; DB 21; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.5e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
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FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      100.0%; Score 909; DB 22; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 6
US-09-724-341-9
; SEQUENCE 9, Application US/09724341
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IQBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/09/724,341
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 9
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-341-9

Query Match      100.0%; Score 909; DB 21; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.5e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
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DB 121 QRSGEVNNNSDNGRYOGL EHRGSEASPALPGLKLSADQVALVYST 166

RESULT 7
PCT-US00-07966-2
; Sequence 2 Application PC/TUS0007966
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT FILING DATE: 2000-03-24
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/126,599
; EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07966-2

Query Match 100.0%; Score 909; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 2,8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELR 120
QY 121 QRSGEVNNNSDNGRYOGL EHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNNSDNGRYOGL EHRGSEASPALPGLKLSADQVALVYST 166

RESULT 9
PCT-US01-19026-22
; Sequence 22 Application PC/TUS0119026
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.; et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253PCT
; CURRENT FILING DATE: 2001-06-14
; CURRENT APPLICATION NUMBER: PCT/US01/19026
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19026-22

Query Match 100.0%; Score 909; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 2,8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELR 120
QY 121 QRSGEVNNNSDNGRYOGL EHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNNSDNGRYOGL EHRGSEASPALPGLKLSADQVALVYST 166

RESULT 9
PCT-US02-16106-46
; Sequence 46 Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT FILING DATE: 2002-05-22
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16106-46

Query Match 100.0%; Score 909; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 2,8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELR 120
QY 121 QRSGEVNNNSDNGRYOGL EHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNNSDNGRYOGL EHRGSEASPALPGLKLSADQVALVYST 166

RESULT 10
US-08-810-572-2
; Sequence 2, Application US/08810572
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572-2

Query Match 100.0%; Score 909; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
DB 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166

RESULT 11
US-09-302-863-2
; Sequence 2, Application US/09302863
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match 100.0%; Score 909; DB 17; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
DB 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572-2

Query Match 100.0%; Score 909; DB 18; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
DB 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166

RESULT 12
US-09-479-856-6
; Sequence 6, Application US/09479856
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75
; CURRENT APPLICATION NUMBER: US/09/479,856
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,068
; EARLIER FILING DATE: 1999-01-07
; EARLIER APPLICATION NUMBER: 60/169,890
; EARLIER FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-479-856-6

Query Match 100.0%; Score 909; DB 19; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
DB 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166

RESULT 13
US-09-533-822-2
; Sequence 2, Application US/09533822
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/09/533,822
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,599
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/188,208
; EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-822-2

Query Match 100.0%; Score 909; DB 19; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
DB 1 MSGLGRSRGGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRVQGLEHRGSEASPALPGLKLSADQVALVYST 166
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Tue Jan 7 10:36:49 2003

us-09-855-158-15.rapm

Page 6

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QY 61 TCAAFCSRSLSCRKQKGFYDHLRLDCISCSICGQHPKQCAVFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKQKGFYDHLRLDCISCSICGQHPKQCAVFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVENNSDNGRYOGLERHRSSEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVENNSDNGRYOGLERHRSSEASPALPGLKLSADQVALVYST 166
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RESULT 14
US-09-569-245-6
; Sequence 6, Application US/09569245
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenteng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75
; CURRENT APPLICATION NUMBER: US/09/569,245
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 293
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-569-245-6
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Query Match 100.0%; Score 909; DB 19; Length 293;
Best Local Similarity 100.0%; Pred. No. 2,8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLGTCTMCKTICNHOSQR 60
Db 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLGTCTMCKTICNHOSQR 60
QY 61 TCAAFCSRSLSCRKQKGFYDHLRLDCISCSICGQHPKQCAVFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKQKGFYDHLRLDCISCSICGQHPKQCAVFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVENNSDNGRYOGLERHRSSEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVENNSDNGRYOGLERHRSSEASPALPGLKLSADQVALVYST 166
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RESULT 15
US-09-627-206-6
; Sequence 6, Application US/09627206
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenteng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75C2
; CURRENT APPLICATION NUMBER: US/09/627,206
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/569,245
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 60
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 293
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-627-206-6
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Query Match 100.0%; Score 909; DB 20; Length 293;
Best Local Similarity 100.0%; Pred. No. 2,8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLGTCTMCKTICNHOSQR 60
Db 1 MSGLGRSRGRGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLGTCTMCKTICNHOSQR 60
QY 61 TCAAFCSRSLSCRKQKGFYDHLRLDCISCSICGQHPKQCAVFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKQKGFYDHLRLDCISCSICGQHPKQCAVFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVENNSDNGRYOGLERHRSSEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVENNSDNGRYOGLERHRSSEASPALPGLKLSADQVALVYST 166
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Search completed: January 7, 2003, 09:53:20
Job time : 279.331 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:38:19 ; Search time 21.6341 Seconds
(without alignments)
543.836 Million cell updates/sec

Title: US-09-855-158-15
Perfect score: 909
Sequence: 1 MSGLGRSRGGRSRVDQER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	909	100.0	166	US-10-293-816-6	Sequence 6, Appli
2	909	100.0	293	US-10-268-951-22	Sequence 22, Appli
3	909	100.0	293	US-10-258-368-1	Sequence 1, Appli
4	909	100.0	293	US-10-293-816-6	Sequence 2, Appli
5	904	99.4	301	US-10-258-368-12	Sequence 12, Appli
6	881	96.9	404	US-10-258-368-15	Sequence 15, Appli
7	851	71.6	366	US-10-258-368-6	Sequence 6, Appli
8	490.5	54.0	334	US-10-258-368-8	Sequence 8, Appli
9	204	22.4	34	PCT-US02-34376-14	Sequence 14, Appli
10	204	22.4	34	US-10-281-053-14	Sequence 14, Appli
11	201	22.1	33	PCT-US02-34376-13	Sequence 13, Appli
12	201	22.1	33	US-10-281-053-13	Sequence 13, Appli
13	97.5	10.7	1548	US-10-180-903-2	Sequence 2, Appli
14	88	9.7	195	US-10-094-886-174	Sequence 174, App
15	88	9.7	195	US-10-094-886-176	Sequence 176, App
16	87.5	9.6	463	US-09-906-777B-285	Sequence 285, App
17	87.5	9.6	463	US-09-904-011C-285	Sequence 285, App
18	87.5	9.6	463	US-09-665-350B-285	Sequence 285, App
19	87.5	9.6	463	US-10-131-813A-360	Sequence 360, App
20	87.5	9.6	463	US-10-131-819A-360	Sequence 360, App
21	87.5	9.6	463	US-10-131-823A-360	Sequence 360, App
22	87.5	9.6	463	US-10-131-824A-360	Sequence 360, App
23	87.5	9.6	463	US-10-131-826A-360	Sequence 360, App
24	87.5	9.6	463	US-10-131-829A-360	Sequence 360, App
25	87.5	9.6	463	US-10-125-936A-360	Sequence 360, App
26	87.5	9.6	463	US-10-127-829A-360	Sequence 360, App

27	87.5	9.6	463	US-10-127-831A-360	Sequence 360, App
28	87.5	9.6	463	US-10-127-835A-360	Sequence 360, App
29	87.5	9.6	463	US-10-127-837A-360	Sequence 360, App
30	87.5	9.6	463	US-10-127-842A-360	Sequence 360, App
31	87.5	9.6	463	US-10-127-850A-360	Sequence 360, App
32	87.5	9.6	463	US-10-127-901A-360	Sequence 360, App
33	87.5	9.6	463	US-10-128-689A-360	Sequence 360, App
34	87.5	9.6	463	US-10-131-830A-360	Sequence 360, App
35	87.5	9.6	463	US-10-131-833A-360	Sequence 360, App
36	87.5	9.6	463	US-10-125-930A-360	Sequence 360, App
37	87.5	9.6	463	US-10-127-825A-360	Sequence 360, App
38	87.5	9.6	463	US-10-127-838B-360	Sequence 360, App
39	87.5	9.6	463	US-10-127-843A-360	Sequence 360, App
40	87.5	9.6	463	US-10-127-849A-360	Sequence 360, App
41	87.5	9.6	463	US-10-128-684A-360	Sequence 360, App
42	87.5	9.6	463	US-10-128-685A-360	Sequence 360, App
43	87.5	9.6	463	US-10-128-686A-360	Sequence 360, App
44	87.5	9.6	463	US-10-128-686A-360	Sequence 360, App
45	87.5	9.6	463	US-10-128-690A-360	Sequence 360, App

ALIGNMENTS

RESULT 1
US-10-293-816-6
; Sequence 6 Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6

Query Match 100.0%; Score 909; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHOSQR 60
Db 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHOSQR 60

Qy 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICSGQHPKQCAIFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICSGQHPKQCAIFCENKLRSPVNLPPELRR 120

Qy 121 QRSGEVENNDSNGRYQGLHRGSEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVENNDSNGRYQGLHRGSEASPALPGLKLSADQVALVYST 166

RESULT 2
US-10-268-951-22
; Sequence 22 Application US/10268951
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2

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/ CURRENT APPLICATION NUMBER: US/10/268,951
/ CURRENT FILING DATE: 2002-10-11
/ PRIOR APPLICATION NUMBER: 10/082,260
/ PRIOR FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/879,919
/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 08/815,783
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: 60/328,401
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/293,812
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,978
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/254,875
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/241,952
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/211,537
/ PRIOR FILING DATE: 2000-06-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO: 22
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-268-951-22
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Query Match
Best Local Similarity 100.0%; Score 909; DB 6; Length 293;
Pred. No. 1,9e-78; Mismatches 0; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
DB 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISASICGQHPKOCAYFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISASICGQHPKOCAYFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
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```
RESULT 3
US-10-258-368-1
/ Sequence 1, Application US/10258368
/ GENERAL INFORMATION:
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Renner, Paul
/ TITLE OF INVENTION: Tacti As As Anti-Tumor Agent
/ FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
/ CURRENT APPLICATION NUMBER: US/10/258,368
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: USSN 60/199,946
/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO: 1
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-258-368-1
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Query Match
Best Local Similarity 100.0%; Score 909; DB 6; Length 293;
Pred. No. 1,9e-78; Mismatches 0; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
DB 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISASICGQHPKOCAYFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISASICGQHPKOCAYFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
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```
RESULT 4
US-10-293-816-2
/ Sequence 2, Application US/10293816
/ GENERAL INFORMATION:
/ APPLICANT: Brum, Richard J.
/ APPLICANT: Von Bulow, Gotz
/ TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
/ FILE REFERENCE: 44158/254623
/ CURRENT APPLICATION NUMBER: US/10/293,816
/ CURRENT FILING DATE: 2002-11-12
/ PRIOR APPLICATION NUMBER: US 09/782,857
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: US 09/290,333
/ PRIOR FILING DATE: 1999-04-12
/ PRIOR APPLICATION NUMBER: US 08/810,572
/ PRIOR FILING DATE: 1997-03-03
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-816-2
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```
Query Match
Best Local Similarity 100.0%; Score 909; DB 6; Length 293;
Pred. No. 1,9e-78; Mismatches 0; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
DB 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISASICGQHPKOCAYFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISASICGQHPKOCAYFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
```

```
RESULT 5
US-10-258-368-12
/ Sequence 12, Application US/10258368
/ GENERAL INFORMATION:
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Renner, Paul
/ TITLE OF INVENTION: Tacti As As Anti-Tumor Agent
/ FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
/ CURRENT APPLICATION NUMBER: US/10/258,368
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: USSN 60/199,946
/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO: 12
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; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-12

Query Match      99.4%; Score 904; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  SGLGSRGRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORT 61
DB  10 SGLGSRGRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORT 69
QY  62 CAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRRQ 121
DB  70 CAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRRQ 129
QY  122 RSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
DB  130 RSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 174

RESULT 6
US-10-258-368-15
; Sequence 15, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-15

Query Match      96.9%; Score 881; DB 6; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.2e-75;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MSGLGSRGRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB  18 MSGLGSRGRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 77
QY  61 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB  78 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 137
QY  121 QRSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQV 160
DB  138 QRSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQV 177

RESULT 7
US-10-258-368-6
; Sequence 6, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
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; PRIOR APPLICATION NUMBER: USN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-6

Query Match      71.6%; Score 651; DB 6; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.8e-54;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MSGLGSRGRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB  24 MSGLGSRGRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 83
QY  61 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNL 115
DB  84 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNL 138

RESULT 8
US-10-258-368-8
; Sequence 8, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-8

Query Match      54.0%; Score 490.5; DB 6; Length 334;
Best Local Similarity 92.6%; Pred. No. 7.9e-39;
Matches 88; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY  25 LW----TGVMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAFCRSLSCRKEQKGFYD 80
DB  13 LWVPGSTG-DVRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAFCRSLSCRKEQKGFYD 71
QY  81 HLLRDCISASICGQHPKQCAFCENKLRSPVNL 115
DB  72 HLLRDCISASICGQHPKQCAFCENKLRSPVNL 106

RESULT 9
PCT-US02-34376-14
; Sequence 14, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: Modified
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
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; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-14

Query Match      22.4%; Score 204; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1,2e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 CRKEQGFYDHLRDCISCAISCGHPKQCAVFC 104
DB 1 CRKEQGFYDHLRDCISCAISCGHPKQCAVFC 34

RESULT 10
; Sequence 14, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86
; CURRENT APPLICATION NUMBER: US/10/281,053
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-14

Query Match      22.4%; Score 204; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1,2e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 CRKEQGFYDHLRDCISCAISCGHPKQCAVFC 104
DB 1 CRKEQGFYDHLRDCISCAISCGHPKQCAVFC 34

RESULT 11
PCT-US02-34376-13
; Sequence 13, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
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; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-13

Query Match      22.1%; Score 201; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2,3e-12;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CPEEQYWDPLGTGCMSCKTCNHQSQRITCAVFC 66
DB 1 CPEEQYWDPLGTGCMSCKTCNHQSQRITCAVFC 33

RESULT 12
US-10-281-053-13
; Sequence 13, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86
; CURRENT APPLICATION NUMBER: US/10/281,053
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-13

Query Match      22.1%; Score 201; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2,3e-12;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CPEEQYWDPLGTGCMSCKTCNHQSQRITCAVFC 66
DB 1 CPEEQYWDPLGTGCMSCKTCNHQSQRITCAVFC 33

RESULT 13
US-10-180-903-2
; Sequence 2, Application US/10180903
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPG6 SERINE PROTEASE GENE DISRUPTIONS,
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
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; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-180-903-2

Query Match 10.7%; Score 97.5; DB 6; Length 1548;
Best Local Similarity 30.2%; Pred. No. 0.45;
Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

QY 14 RVDDQ--ERRPQGLWTGVAMRSCPEEQYWDPLLG-TCMSCKTICN-----HQSQTCAAF 65
DB 627 RADKHGQERF--LVHGECLNCPVGHY--PAKGHITCLFPCDNCCLYNPHICRMSGY 681

QY 66 -----CRSLSCRKEQGFYDHLRLDCISCASIC 93
DB 682 VIIPNHTCQKLECR--QGEFQDSEYECMPCBEGC 715

RESULT 14
US-10-094-886-174
; Sequence 174, Application US/10094886
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangolli, Esha
; APPLICANT: Gusev, Vladimir
; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderina, Steven
; APPLICANT: LaRochele, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094,886
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281

; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 174
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-174

Query Match 9.7%; Score 88; DB 6; Length 195;

Best Local Similarity 26.0%; Pred. No. 0.54;
Matches 39; Conservative 15; Mismatches 50; Indels 46; Gaps 10;

QY 28 GVAMRSCPEEQYWD--PLLGTCMCKTICNHQSQTCAAFCSRSLSCRKEQGFYDHL--- 82
DB 55 GVCLLSCPSGVGYTRYDPDINKTKCADCD-----TC--FNKNF-CTKCKSGFYHLGKC 106

QY 83 LRDC-----ISCASI-----CGOHPKOCAY--FCENKLRSPV----- 112
DB 107 LDNCPGLEANNHTMECVSIVHCEVSEWNPSPCTKKGKTCGFKGTETRVRETIQHPSA 166

QY 113 --NLPPELRQRSGEVNDSNDRYOGLE 140
DB 167 KGNLCPTNETRKTCTVORKKCKQGE--KGLE 195

RESULT 15
US-10-094-886-176
; Sequence 176, Application US/10094886
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangolli, Esha
; APPLICANT: Gusev, Vladimir
; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderina, Steven
; APPLICANT: LaRochele, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B

Tue Jan 7 10:36:50 2003

us-09-855-158-15.rapn

Page 6

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; CURRENT APPLICATION NUMBER: US/10/094,886
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn 2.1
; SEQ ID NO: 176
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-176
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Query Match          9 7%; Score 88; DB 6; Length 195;
Best Local Similarity 26.0%; Pred. No. 0.54; 50; Indels 46; Gaps 10;
Matches 39; Conservative 15; Mismatches 50; Indels 46; Gaps 10;

QY 28 GVMRSGPBEQYWD--PLGTGMSCKTICNHQSORTCAAFGRSLSCRKQKFTYDHL--- 82
DB 55 GVCLSGSPSGYGTGRYPDINKCTKCRACD-----TC--FNKNF--CTKCKSGFYHLHGKC 106
QY 83 LRDC-----ISCASI-----CGQHPKQCAV--PCENKLRSPV----- 112
DB 107 LDNCPGEGLEANNHTMECVSIHCEVSEWNPSPCTGKKGKGTGFGRTETRVREIIQHPSA 166
QY 113 --NLPELRRRSGEVEENNNSDNGRYGLE 140
DB 167 KGNLCPTNETRKTCTVQRKKCKQGE--RGLE 195
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Search completed: January 7, 2003, 09:54:18
Job time : 22.6341 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:39 ; Search time 24.0125 Seconds
(without alignments)
371.797 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405

Sequence: 1 CPBEQWPLLTGTCMSCKTI.....DCISCASICGHPKQCAFYC 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	97.0	166	19 AAW75785	Human lymphocyte s
2	393	97.0	166	23 AAE15494	Human TACI extrace
3	393	97.0	265	22 AAE09244	Human TACI splice
4	393	97.0	291	23 AAU10949	Human AGP-3 recept
5	393	97.0	293	19 AAW75783	Human lymphocyte s
6	393	97.0	293	21 AAB36312	Human neutrokine s
7	393	97.0	293	21 AAY94000	A transmembrane ac
8	393	97.0	293	22 AAE09240	Human TACI protein
9	393	97.0	293	22 AAY71914	Human tumour necro
10	393	97.0	293	23 AAU95912	Human TACI-Ig Fc

11	393	97.0	293	23 ABB81488	Human TACI recepto
12	393	97.0	293	23 AA014130	Human transmembran
13	393	97.0	293	23 AAU75408	Tumour necrosis fa
14	393	97.0	293	23 AAE15493	Human transmembran
15	393	97.0	293	23 AAU09800	Human AGP-3 relate
16	393	97.0	342	23 AAU09335	Protein of N-termin
17	393	97.0	334	23 AA014133	Protein of hTACI (
18	393	97.0	386	23 AA014132	Protein of hTACI (
19	393	97.0	357	23 AAE15498	Human TACI-immunog
20	393	97.0	404	23 AA014136	Protein of a compl
21	313	77.3	59	23 AAE15500	Human TACI cystein
22	256	63.2	249	21 AAY94006	A murine znf4, a
23	204	50.4	34	23 AAE15496	Human TACI cystein
24	204	50.4	38	23 AAU10952	Human AGP-3 recept
25	204	50.4	247	21 AAY93398	Human BR43x2, an i
26	201	49.6	33	23 AAE15495	Human TACI cystein
27	201	49.6	37	23 AAU10951	Human AGP-3 recept
28	84.5	20.9	220	22 AAB65001	Human secreted pro
29	76.5	18.9	325	19 AAW53240	Homo sapiens vascu
30	76.5	18.9	325	22 AAY97372	Human VEGF-D prote
31	76.5	18.9	354	19 AAW49036	Human vegf2 growt
32	76.5	18.9	354	19 AAW53241	Homo sapiens vascu
33	76.5	18.9	354	19 AAW44293	Human vascular end
34	76.5	18.9	354	21 AAB10649	Human VEGD protein
35	76.5	18.9	354	21 AAB29049	Human VEGF-D prote
36	76.5	18.9	354	21 AAY70750	Human prepro-vascu
37	76.5	18.9	354	21 AAY70983	Human vascular end
38	76.5	18.9	354	22 AAU08441	Polypeptide for hu
39	76.5	18.9	354	22 AAB70685	Human vascular end
40	76.5	18.9	354	22 AAY97573	Human VEGF-D1 prot
41	76.5	18.9	354	22 AAB37606	Human VEGF-D; Hom
42	76.5	18.9	620	18 AAW14594	Human VEGF-D; induc
43	76	18.8	173	21 AAY77467	Human Rank-like pr
44	76	18.8	173	22 AAU03118	Composite protein
45	76	18.8	197	21 AAB01421	Human TANGO 140-2.

ALIGNMENTS

RESULT 1
AAW75785
ID AAW75785 standard; Protein; 166 AA.
AC AAW75785;
XX
XX
DT 18-JAN-1999 (first entry)
XX
DE Human lymphocyte surface receptor extracellular domain.
XX
XX
KW TACI; transmembrane activator and CAML-interactor;
KW calcium signal-modulating cyclophilin ligand; human,
KW lymphocyte surface receptor; human B-cell; a lymphocyte;
KW infection; cancer; rheumatoid arthritis; autoimmune disease;
KW glomerulonephritis; immunosuppressive; graft versus host disease;
KW transplant rejection; therapy; signal transduction.
XX
OS Homo sapiens.
XX
PN WO9839361-A1.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US04270.
XX
PR 03-MAR-1997; 97US-0810572.
XX
PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Bram RJ, Von Bulow G;
XX
DR WPI; 1998-506346/43.
DR N-PSDB; AAV57330.

XX New isolated transmembrane activator protein - used to develop
PT products for treating e.g. infections, cancers, autoimmune and
PT inflammatory conditions, transplant rejection or graft-versus-host
PT disease
XX
PS Claim 8; Page 73; 89pp; English.
XX
CC This is the amino acid sequence of the N-terminal, i.e. the
CC extracellular, domain of novel human transmembrane activator and
CC CAML-interactor (TACI) protein (see AAW75783). TACI is a lymphocyte
CC receptor protein that is involved in the calcium activation pathway.
CC It is normally present in B-lymphocytes, and to a much lesser extent
CC in immature T-lymphocytes, and can therefore be targeted to
CC specifically regulate B cell responses without affecting T cell
CC activity. The extracellular domain of TACI functions as a binding
CC site for a ligand that stimulates the activation of the cell by
CC inducing the binding of the C-terminal portion (see AAW75784) of
CC TACI to the N-terminal domain of CAML. A recombinant form of the
CC extracellular portion of TACI acts as a dominant-negative or
CC blocking agent and acts to suppress the immune system. It can be
CC used to treat or prevent autoimmune disease, graft rejection or
CC graft versus host disease. The extracellular region is also used
CC in a claimed method for identifying a ligand for TACI, in which
CC binding of a candidate molecule is determined by detecting cellular
CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT
CC transcription factor, or of NF-AT dependent transcription.
CC
XX
SQ Sequence 166 AA;
Query Match 97.0%; Score 393; DB 19; Length 166;
Best Local Similarity 94.4%; Pred. No. 7,7e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMSCKTICNHOSORTCAFC----CRKEQKGFYDHLRDCISCASIC 56
DB 34 CPEEQYWDPLLTGTCMSCKTICNHOSORTCAFCRSLSCKEKGKFDHLRDCISCASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104
RESULT 2
AAE15494
ID AAE15494 standard; Protein; 166 AA.
XX
AC AAE15494;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human TACI extracellular domain.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
PR

XX (AMGE-) AMGEN INC.
XX
XX The11 LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
PS Claim 1; Fig 12A; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (g70, a tumour necrosis factor-TNF
CC family ligand), having the consensus sequence region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma), hyperemesis, Crohn's
CC disease) drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis) scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI protein extracellular domain.
XX
SQ Sequence 166 AA;
Query Match 97.0%; Score 393; DB 23; Length 166;
Best Local Similarity 94.4%; Pred. No. 7,7e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMSCKTICNHOSORTCAFC----CRKEQKGFYDHLRDCISCASIC 56
DB 34 CPEEQYWDPLLTGTCMSCKTICNHOSORTCAFCRSLSCKEKGKFDHLRDCISCASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104
RESULT 3
AAE09244
ID AAE09244 standard; Protein; 265 AA.
XX
AC AAE09244;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human TACI splice variant protein.
XX
KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200160397-A1.
XX
PD 23-AUG-2001.
XX
PF 28-NOV-2000; 2000WO-US32378.
XX 16-FEB-2000; 2000US-0182938.
XX


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PR 22-AUG-2000; 2000US-0226986.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
XX Yan M;
XX WPI; 2001-541628/60.
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
XX activity, for treating autoimmune disorders and cancer, comprises
XX exposing the cells to TALL-1 or APRIL polypeptide agonists or
XX antagonists -
XX
XX Example 1; Fig 6; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
XX antagonists to modulate the activity of the members of TNF (tumour
XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
XX e.g. TACI or BCMA. The method is useful for treating pathological
XX conditions or diseases associated with increased TALL-1 and APRIL
XX expression or activity. TALL-1 and APRIL antagonists are used to
XX block the interaction between APRIL and TALL-1 with TACI or BCMA.
XX They are useful for treating a mammal suffering from cancer such
XX as leukaemia, lymphoma, myeloma, cancers of lung and colon and
XX autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
XX psoriasis and lupus erythematosus. The present sequence is human
XX TACI splice variant protein.
XX
XX Sequence 265 AA;
XX
XX Query Match 97.0%; Score 393; DB 22; Length 265;
XX Best Local Similarity 94.4%; Pred. No. 1.2e-32;
XX Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
XX
XX QY 1 CPBEQYWDPLGLTGMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
XX Db 34 CPBEQYWDPLGLTGMCKTICNHQSORTCAAFCSRSLSCREQGFYDHLRLDCISCASIC 93
XX
XX QY 57 GQHPKQCAVFC 67
XX Db 94 GQHPKQCAVFC 104
XX
XX RESULT 4
XX AAU10949
XX ID AAU10949 standard; Protein; 291 AA.
XX AC AAU10949;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Human AGP-3 receptor extracellular domain.
XX
XX KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
XX dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
XX antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
XX antiParkinsonian; antiparotatic; vasotropic; antibacterial; asthma;
XX AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
XX mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
XX rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
XX pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
XX diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
XX multiple sclerosis; Parkinson's disease; transgenic animal.
XX
XX OS Homo sapiens.
XX
XX PN WO200185782-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 12-FEB-2001; 2001WO-US04568.
XX

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PR 11-FEB-2000; 2000US-181800P.
XX (AMGE-) AMGEN INC.
XX Boyle WJ, Hsu H;
XX WPI; 2002-049441/06.
XX
XX Composition, useful for identifying modulator of receptor for treating
XX asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
XX ligand family member) receptor and encoding nucleic acids -
XX
XX Claim 1; Fig 18; 124pp; English.
XX
XX The invention relates to a composition (I) comprising AGP-3 receptor
XX (tumour necrosis factor ligand family member) related protein (II)
XX attached to a vehicle protein. (I) is useful for modulating AGP-3-related
XX activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
XX assays to identify cells and tissues that express AGP-3R or proteins
XX related to AGP-3R-related protein and for identifying compounds
XX (agonists or antagonists) that interact with AGP-3R proteins. (II) is
XX also useful for identifying intracellular proteins that interact with
XX the respective cytoplasmic domains by yeast two-hybrid screening
XX process. (II) is involved in B cell growth, survival and activation
XX particularly in lymph node, spleen, and Peyer's patches. AGP-3R
XX agonists and antagonists identified using (II) are used for modulating
XX B cell response and are used to treat diseases characterised by
XX inflammatory processes or deregulated immune response such as
XX rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
XX lupus etc. (II) is also useful in the production of hybridoma cells
XX which are derived from B cells which involves treating the hybridoma
XX cells with (II). (II) is useful in the treatment of inflammatory
XX conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
XX (II), its agonists or antagonists are useful for treating acute
XX pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
XX asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
XX glomerulonephritis, inflammatory bowel disease, ischaemic injury
XX including cerebral ischaemia, multiple myeloma, multiple sclerosis,
XX osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
XX shock, etc. The nucleic acids are also useful for developing transgenic
XX animals expressing (II), which are useful for producing the polypeptides
XX and for the study of in vivo biological activity. The present sequence
XX represents the amino acid sequence of human AGP-3 extracellular domain.
XX
XX Sequence 291 AA;
XX
XX Query Match 97.0%; Score 393; DB 23; Length 291;
XX Best Local Similarity 94.4%; Pred. No. 1.3e-32;
XX Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
XX
XX QY 1 CPBEQYWDPLGLTGMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
XX Db 34 CPBEQYWDPLGLTGMCKTICNHQSORTCAAFCSRSLSCREQGFYDHLRLDCISCASIC 93
XX
XX QY 57 GQHPKQCAVFC 67
XX Db 94 GQHPKQCAVFC 104
XX
XX RESULT 5
XX AAU75783
XX ID AAU75783 standard; Protein; 293 AA.
XX AC AAU75783;
XX
XX DT 18-JAN-1999 (first entry)
XX
XX DE Human lymphocyte surface receptor TACI.
XX
XX KW TACI; transmembrane activator and CAML-interactor;
XX calcium signal-modulating cyclophilin ligand; human;
XX lymphocyte surface receptor; human; B-cell; B lymphocyte;
XX infection; cancer; rheumatoid arthritis; autoimmune disease;
XX

```


ID AAY94000 standard; Protein; 293 AA.
AC AAY94000;
XX
XX
DT 20-OCT-2000 (first entry)
XX
XX
DE A transmembrane activator and CAML-interactor (TACI).
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
OS Homo sapiens.
XX
XX WO200040716-A2.
XX
XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
PI WPI; 2000-452538/39.
DR N-PSDB; AAA58558.
XX
XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
PS Disclosure; Page 149-150; 175pp; English.
XX
XX The present sequence represents a human transmembrane activator and
CC CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
CC or BCMA (a related B cell protein) receptor contain a cysteine rich
CC domain, and are used for inhibiting ztnf4 activity. ztnf4 is a TNF
CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA
CC receptor-ligand engagement associated with activated or resting B
CC lymphocytes, effector T-cells, or with antibody production. The
CC antibody production is associated with an autoimmune disease selected
CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
CC and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA
CC receptor-ligand engagement is associated with asthma, bronchitis,
CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
CC light chain neuropathy, amyloidosis, moderating immune response,
CC immunosuppression, graft rejection, graft versus host disease,
CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
CC polypeptides, fusions, antibodies, agonists or antagonists can be used
CC to treat hypertension, renal artery stenosis, or occlusion, and
XX cholesterol or renal emboli.

Sequence 293 AA;

Query Match 97.0%; Score 393; DB 21; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.3e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPBEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSLSCRKEQKGFYDHLRLDCISCASIC 56
|||||

Db 34 CPBEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSLSCRKEQKGFYDHLRLDCISCASIC 93
QY 57 GQHPKQCAAYFC 67
|||||
Db 94 GQHPKQCAAYFC 104
|||||

RESULT 8

AAE09240
ID AAE09240 standard; Protein; 293 AA.

AC AAE09240;

XX 19-NOV-2001 (first entry)

DT Human TACI protein.

DE Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;

KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;

KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;

KW psoriasis.

XX Homo sapiens.

XX WO200160397-A1.

PN 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US32378.

XX 16-FEB-2000; 2000US-0182938.

XX 22-AUG-2000; 2000US-0226986.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;

XX Yan W;

XX WPI; 2001-541628/60.

XX N-PSDB; AADI5901.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological

PT activity, for treating autoimmune disorders and cancer, comprises

PT exposing the cells to TALL-1 or APRIL polypeptide agonists or

PT antagonists -

XX Example 1; Fig 1; 160pp; English.

XX The invention relates to methods of using one or more agonists or

CC antagonists to modulate the activity of the members of TNF (tumour

CC necrosis factor), especially TALL-1, APRIL and TNF receptor (TNFR)

CC e.g. TACI or BCMA. The method is useful for treating pathological

CC conditions or diseases associated with increased TALL-1 and APRIL

CC expression or activity. TALL-1 and APRIL antagonists are used to

CC block the interaction between APRIL and TALL-1 with TACI or BCMA.

CC They are useful for treating a mammal suffering from cancer such

CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and

CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,

CC psoriasis and lupus erythematosus. The present sequence is human

CC TACI protein.

XX Sequence 293 AA;

QY 1 CPBEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSLSCRKEQKGFYDHLRLDCISCASIC 56
|||||

Db 34 CPBEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSLSCRKEQKGFYDHLRLDCISCASIC 93
|||||

QY 57 GQHPKQCAAYFC 67
|||||

Query Match 97.0%; Score 393; DB 22; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.3e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

DB 94 GQHPKQCAVFC 104

RESULT 9

AA71914

ID AA71914 standard; Protein; 293 AA.

XX

AC AA71914;

XX

DT 26-MAR-2001 (first entry)

XX

DE Human tumour necrosis factor receptor (TACI) protein.

XX

KW Human; transmembrane activator and CAML interactor; TACI; tumour necrosis factor receptor; TNF; autoimmune disease; diabetes; calcium-signal modulating cyclophilin ligand; CAML; viral infection; neurokinin alpha polypeptide; TACI-Ligand; TACI-L; cytosolic; therapy; neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour; anarthritic; antineumatic; immunosuppressive; multiple sclerosis; rheumatoid arthritis; graft rejection; inflammation; cell proliferation; cell death; immunoglobulin E-mediated allergic reaction; IGE.

XX

OS Homo sapiens.

XX

PH Key

FT Domain

FT 2..166 Extracellular domain

FT /Notes "Binds with amino acids 123-285 of extracellular domain of TACI-L"

XX

PN WO200067034-A1.

XX

PD 09-NCV-2000.

XX

PF 14-APR-2000; 2000WO-US10282.

XX

PR 30-APR-1999; 99US-0302863.

XX

PA (IMMU) IMMUNEX CORP.

XX

PI Goodwin RG, Din WS;

XX

DR WPI; 2001-016005/02.

XX

DR N-PSDB; AAD02006.

XX

PT Use of new interactions between tumour necrosis factor receptors (TACI) and TACI ligands to screen candidate molecules for determining agonist and antagonist interactions which are used for treating inflammation -

XX

PS Claim 10; Fig 1b; 46pp; English.

XX

CC The present sequence is a human tumour necrosis factor receptor (TACI) protein. TACI (Transmembrane activator and calcium-signal modulating cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L complex is useful for modulating an intracellular signalling cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are used to inhibit the interaction between TACI and TACI-L for therapeutic purposes to treat tumour and tumour metastasis and to combat various autoimmune diseases e.g. multiple sclerosis and diabetes, as well as other disorders, such as viral infection, rheumatoid arthritis, graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions and inflammation. The interaction is used to study cellular processes associated with tumour necrosis factor (TNF)-receptors such as immune regulation, cell proliferation, cell death and inflammatory responses. CC The interaction between the extracellular region of TACI and TACI-L can be used to further develop understanding of which cell types TACI-L acts upon.

XX

SO Sequence 293 AA;

Query Match 97.0%; Score 393; DB 22; Length 293;

Best Local Similarity 94.4%; Pred. No. 1.3e-32;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYMDPLIGTCTMCSCTICNHSQRTCAAPC-----CRKQCKFYHLLADPCLSCASIC 56

DB 34 CPEQYMDPLIGTCTMCSCTICNHSQRTCAAPCRLSLCKRQKGYDHLNDCLSCASIC 93

QY 57 GQHPKQCAVFC 67

DB 94 GQHPKQCAVFC 104

RESULT 10

AAU99512

ID AAU99512 standard; Protein; 293 AA.

XX

AC AAU99512;

XX

DT 07-OCT-2002 (first entry)

XX

DE Human TACI-IgG Fc fusion protein.

XX

KW Human; tumour necrosis factor; TNF delta; pulmonary system disorder; immunoglobulin production; B-cell proliferation; immune system disorder; autoimmune disease; cancer; lymphoproliferative disorder; pain; microbial infection; parasitic infection; bone disease; atherosclerosis; cardiovascular disease; neurodegenerative disease; wound healing; graft versus host disease; haematopoietic cell disorder; nephritis; transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG; immunoglobulin G; Fc portion.

XX

OS Homo sapiens.

XX

PN US2002064829-A1.

XX

PD 30-MAY-2002.

XX

PF 14-JUN-2001; 2001US-0879919.

XX

PR 14-MAR-1996; 96US-016812P.

XX

PR 15-JUN-2000; 2000US-211537P.

XX

PR 23-OCT-2000; 2000US-241952P.

XX

PR 13-DEC-2000; 2000US-254875P.

XX

PR 16-MAR-2001; 2001US-276248P.

XX

PR 23-MAR-2001; 2001US-277978P.

XX

PR 25-MAY-2001; 2001US-293499P.

XX

PR 12-MAR-1997; 97US-0815763.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Yu G, Ni J, Gentz RL, Dillon PJ;

XX

DR WPI; 2002-556722/59.

XX

PT Novel human multimeric tumour necrosis factor delta or epsilon protein useful for treating disease or disorder of immune system such as autoimmune disease, immunodeficiency, or cancer of immune system -

XX

PS Example 29; Page 125; 143pp; English.

XX

CC The present invention relates to the isolation of human tumour necrosis factor (TNF) delta and TNF epsilon proteins, and the polynucleotide sequences encoding them. The proteins are useful for modulating immunoglobulin production or for modulating proliferation of B-cells. CC The sequences of the invention are useful for treating diseases or disorders of the immune system. Such disorders include autoimmune diseases (e.g. systemic lupus erythematosus (SLE), acquired immunodeficiency syndrome (AIDS)), cancers of the immune system (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma, non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative disorders, microbial infections (e.g. viral, bacterial), parasitic infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis, pain, cardiovascular disorders (e.g. myocardial infarction, stroke), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's

CC disease), graft versus host disease, wound healing, haematopoietic cell
 CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma), of the
 CC diseases (e.g. anorexia, inflammatory disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence for human
 CC transmembrane activator and CAML-interactor (TACI)-immunoglobulin G
 CC (IgG) Fc fusion protein is used in the examples of the present
 CC invention.

XX Sequence 293 AA;
 SQ

Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. NO. 1.3e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFPC----CRKEQKGFYDHLRLDCISCASIC 56
 DB 34 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCASIC 93
 QY 57 GQHPKQCAAYFC 67
 DB 94 GQHPKQCAAYFC 104

RESULT 11
 ID ABB81488 standard; Protein; 293 AA.
 AC ABB81488;
 DT 02-SEP-2002 (first entry)
 DE Human TACI receptor related protein SEQ ID NO:8.
 KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; anti-inflammatory; antidiabetic;
 KW neuroprotective; anti-rheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200238766-A2.
 PD 16-MAY-2002.
 XX
 XX 05-NOV-2001; 2001WO-US47018.
 XX
 XX 07-NOV-2000; 2000US-246449P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 PI WPI; 2002-508212/54.
 DR
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 XX Disclosure; Page 136-137; 154pp; English.
 PS
 XX The present invention describes a human tumour necrosis factor receptor

CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive;
 CC dermatological, anti-inflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating production of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.

XX Sequence 293 AA;
 SQ

Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. NO. 1.3e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFPC----CRKEQKGFYDHLRLDCISCASIC 56
 DB 34 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCASIC 93
 QY 57 GQHPKQCAAYFC 67
 DB 94 GQHPKQCAAYFC 104

RESULT 12
 ID AAO14130 standard; Protein; 293 AA.
 AC AAO14130;
 XX
 DT 02-MAY-2002 (first entry)
 XX
 XX Human transmembrane activator CAML interactor protein (TACI).
 DE
 XX Human transmembrane activator CAML interactor protein; TACI; cytostatic;
 KW cell proliferation; tumour; vulnary; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
 KW uterine.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Domain 1..114
 FT /label= Extracellular_domain
 XX
 XX WO200181417-A2.
 XX
 XX 01-NOV-2001.
 XX
 XX 27-APR-2001; 2001WO-US40626.
 XX
 XX 27-APR-2000; 2000US-199946P.
 PR
 XX (BIOJ) BIOGEN INC.
 XX (APOT-) APOTEC R & D SA.
 XX
 XX Ambrose C, Thompson J, Schneider P, Rennert P;

XX WPI; 2002-062027/08.
 DR N-PSDB; AAK98726.
 XX
 PT Treating mammal for condition associated with undesired cell
 PT proliferation e.g., solid tumour or reducing solid tumour size located in
 PT mammal comprises administering transmembrane activator CAML interactor
 PT protein reagent
 XX
 XX Claim 8; Fig 1, 42pp; English.
 XX
 XX This sequence represents the human transmembrane activator CAML
 CC interactor protein (TACI). The invention relates to treating a mammal for
 CC a condition associated with undesired cell proliferation (e.g. a solid
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)
 CC comprising administering a transmembrane activator CAML interactor
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnereary
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
 CC cat) for a condition associated with undesired cell proliferation (e.g.
 CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
 CC cancer). The method is also useful for treating cellular
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
 CC rheumatoid arthritis, post-surgical scarring and lung liver and urethra
 CC fibrosis. The TACI reagent of the invention can extend mean survival time
 CC of a mammal by 25% as compared to the mean survival time of a mammal in
 CC the absence of administering the TACI reagent. The TACI reagent also
 CC reduces the size of the tumour by 25% or more.
 CC
 XX Sequence 293 AA;
 SQ
 Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. No. 1.3e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 CPEEQYWPDLGTGCMSCRTICNHOSORTCAFC-----CRKQKGFYDHLRDICISCSASIC 56
 DB 34 CPEEQYWPDLGTGCMSCRTICNHOSORTCAFCRSISCRKQKGFYDHLRDICISCSASIC 93
 QY 57 GQHPKQCAVFC 67
 DB 94 GQHPKQCAVFC 104
 RESULT 13
 AAU75408 standard; Protein; 293 AA.
 ID AAU75408;
 AC XX
 XX 09-APR-2002 (first entry)
 DT XX
 XX Tumour necrosis factor (TNF) receptor TACI-FC fusion.
 DE XX
 XX Tumour necrosis factor; TNF; cytostatic; arteriosclerosis;
 KW analgesic; cerebroprotective; neurotropic; neuroprotective; hepatotropic;
 KW immunoglobulin production; B cell proliferation; immunosuppressive;
 KW HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
 KW Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
 KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
 KW acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
 KW chronic lymphocytic leukemia; lymphoproliferative disorder;
 KW bacterial infection; viral infection; osteoporosis; atherosclerosis;
 KW pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
 KW neurodegenerative disease; inflammation; liver disease; cirrhosis;
 KW cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
 KW ulcerative colitis; angioneitis; septic shock; wound healing;
 KW tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
 XX
 XX Homo sapiens.
 OS Synthetic.

XX WO200196528-A2.
 XX
 XX 20-DEC-2001.
 PD XX
 XX
 XX 14-JUN-2001; 2001WO-US19026.
 PF XX
 XX 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
 XX WPI; 2002-130727/17.
 XX N-PSDB; ABR13415.
 DR
 XX Novel multimeric human tumour necrosis factor delta or epsilon protein
 PT useful for treating cancer, immune system disorders, infection,
 PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
 PT psoriasis
 PT
 PS Example 29; Page 341-342; 344pp; English.
 XX
 XX The invention describes a multimeric human tumour necrosis factor (TNF)
 CC delta or epsilon protein (I). (I) or a composition containing them (II)
 CC are useful for modulating immunoglobulin production or proliferation of B
 CC cells. (I) or (II) is useful for treating a disease or disorder of the
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
 CC lymphoma, multiple myeloma and chronic lymphocytic leukemia (CLL)); in
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
 CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
 CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
 CC angiogenesis and wound healing; as a diagnostic research reagent; as an
 CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
 CC receptor; in apoptosis of transformed cell lines; mediation of cell
 CC activation and proliferation; and as an immunogen to produce (II). (II)
 CC is useful to purify, detect and target (I), for measuring levels of (I)
 CC in biological samples, for immunophenotyping samples, and to treat,
 CC inhibit or prevent diseases and disorders associated with aberrant
 CC expression and/or activity of (I). This is the amino acid sequence of a
 CC fusion protein of tumour necrosis factor receptor TNFRI and immunoglobulin
 CC G (Igg) crystallisation fragment, described in the method of the
 CC invention.
 XX
 XX Sequence 293 AA;
 SQ
 Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. No. 1.3e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 CPEEQYWPDLGTGCMSCRTICNHOSORTCAFC-----CRKQKGFYDHLRDICISCSASIC 56
 DB 34 CPEEQYWPDLGTGCMSCRTICNHOSORTCAFCRSISCRKQKGFYDHLRDICISCSASIC 93
 QY 57 GQHPKQCAVFC 67
 DB 94 GQHPKQCAVFC 104
 RESULT 14
 ABR15493 standard; Protein; 293 AA.
 ID ABR15493

XX AAE15493;
 XX
 XX 12-MAR-2002 (first entry)
 XX
 XX Human transmembrane activator and intracellular CAML interactor protein.
 XX
 XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 XX Region 34..66
 FT /note= "Cysteine-rich consensus region"
 FT Region 71..104
 FT /note= "Cysteine-rich consensus region"
 FT Domain 167..186
 FT /label= Transmembrane_domain
 XX
 XX WO200187979-A2.
 DN
 XX
 XX 22-NOV-2001.
 PD
 XX
 XX 14-MAY-2001; 2001WO-US15567.
 PF
 XX
 XX 12-MAY-2000; 2000US-204039P.
 PR
 XX 27-JUN-2000; 2000US-214591P.
 PR
 XX 14-MAY-2001; 2001US-0214591.
 PR
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Theall LE, Yu G;
 PI
 XX
 XX WPI; 2002-066686/09.
 DR
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 PT
 XX
 XX Disclosure; Fig 12A; 94pp; English.
 PS
 XX
 XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human TACI protein.
 XX
 XX Sequence 293 AA;
 SQ

Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. No. 1.3e-32;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 CPESQYMDPLLTGTCMSCKTICNHQSQTCAAF-----CRKEQGFYDHLRDCISCASIC 56
 DB 34 CPESQYMDPLLTGTCMSCKTICNHQSQTCAAF-----CRKEQGFYDHLRDCISCASIC 93
 QY 57 GOHPKQCAAYFC 67
 DB 94 GOHPKQCAAYFC 104
 RESULT 15
 AAU09900
 ID AAU09900 standard; Protein; 293 AA.
 XX
 XX AAU09900;
 XX
 XX 12-MAR-2002 (first entry)
 XX
 XX Human AGP-3 related protein receptor.
 XX
 XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 KW dermatological; neuroprotective; neutropic; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 KW mesenteric lymph node; AGP-3; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200185782-A2.
 FN
 XX
 XX 15-NOV-2001.
 XX
 XX 12-FEB-2001; 2001WO-US04568.
 PF
 XX
 XX 11-FEB-2000; 2000US-181800P.
 PR
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Boyle WJ, Hsu H;
 PI
 XX
 XX WPI; 2002-049441/06.
 DR
 XX N-FSD5; AAS18558.
 DR
 XX
 XX Composition, useful for identifying modulator of receptor for treating
 PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
 PT ligand family member) receptor and encoding nucleic acids -
 XX
 XX Disclosure; Page 117-119; 124pp; English.
 XX
 XX The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumour necrosis factor ligand family member) related protein (II)
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds
 CC (agonists or antagonists) that interact with AGP-3R proteins. (II) is
 CC also useful for identifying intracellular proteins that interact with
 CC the respective cytoplasmic domains by yeast two-hybrid screening
 CC process. (II) is involved in B cell growth, survival and activation
 CC particularly in lymph node, spleen, and Peyer's patches. AGP-3R
 CC agonists and antagonists identified using (II) are used for modulating
 CC B cell response and are used to treat diseases characterised by
 CC inflammatory processes or deregulated immune response such as
 CC rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
 CC lupus, etc. (II) is also useful in the production of hybridoma cells
 CC which are derived from B cells, which involves treating the hybridoma
 CC cells with (II). (II) is useful in the treatment of inflammatory

CC conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
 CC (ii), its agonists or antagonists are useful for treating acute
 CC pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
 CC glomerulonephritis, inflammatory bowel disease, ischemic injury
 CC including cerebral ischemia, multiple myeloma, multiple sclerosis,
 CC osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
 CC shock, etc. The nucleic acids are also useful for developing transgenic
 CC animals expressing (ii), which are useful for producing the polypeptides
 CC and for the study of in vivo biological activity. The present sequence
 CC represents the amino acid sequence of human Agp-3 related protein
 CC receptor.
 CC
 XX
 SQ Sequence 293 AA;

Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. No. 1.3e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY	1	CPEEQYWDPLGTOMSKTICNHOSORTCAFC---	CRKEQGFYDHLRDCISCASIC	56
DB	34	CPEEQYWDPLGTOMSKTICNHOSORTCAFCRSLS	CRKEQGFYDHLRDCISCASIC	93
QY	57	GOHPKQCAVFC		67
DB	94	GOHPKQCAVFC		104

Search completed: January 7, 2003, 09:37:29
 Job time : 25.0125 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 9.57143 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405
Sequence: 1 CPBEQYWDPLGTCMSCKTI.....DCISCASICGHPKQCAAYFC 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_73:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	81.5	20.1	1299	2	T43251	furin (EC 3.4.21.75) - fall armyworm
2	80	19.8	1108	2	H69834	hypothetical prote
3	77	19.0	2664	2	T28626	variant-specific s
4	75	18.5	1548	2	S34583	serine proteinase
5	74.5	18.4	962	2	JC5571	subtilisin-like pr
6	74.5	18.4	969	1	A39490	subtilisin-like pr
7	74.5	18.4	975	2	JC5570	subtilisin-like pr
8	71.5	17.7	773	2	I46059	beta-1 integrin su
9	71.5	17.7	932	2	I52527	PACE4A - mouse (fr
10	71.5	17.7	1680	2	A43434	furin (EC 3.4.21.7
11	71	17.5	108	2	AD0715	conserved hypothet
12	70	17.3	1124	1	I58388	protein-tyrosine k
13	69.5	17.2	798	2	S01659	integrin beta-1 ch
14	69.5	17.2	799	1	IQM5FB	fibronectin recept
15	69	17.0	899	2	G02428	subtilisin-like pr
16	69	17.0	915	2	JG6148	subtilisin-like pr
17	68.5	16.9	501	2	I61512	TNF receptor assoc
18	68	16.8	1339	2	JC4387	epidermal growth f
19	67.5	16.7	146	2	S46368	surface protein 51
20	67.5	16.7	2233	2	T28669	STIG1 protein - co
21	67.5	16.7	3084	1	MMWSA	laminin alpha-1 ch
22	67	16.5	1210	1	AS3183	epidermal growth f
23	67	16.5	1751	1	MGHUMH	laminin alpha-2 ch
24	66.5	16.4	184	2	S34586	B-cell maturation
25	66.5	16.4	937	2	I53282	gene PAC84 protein
26	66	16.3	248	2	T03869	hypothetical protei
27	66	16.3	1119	2	A88481	protein C16A3.6 [i
28	66	16.3	1122	2	I54237	protein-tyrosine k
29	66	16.3	1123	1	JN0712	protein-tyrosine k

30 66 16.3 1125 1 JH0771 protein-tyrosine k
31 66 16.3 1210 1 GQHUE epidermal growth f
32 65.5 16.2 202 2 T50635 hypothetical prote
33 65.5 16.2 210 2 T33697 hypothetical prote
34 65.5 16.2 843 2 A27131 epidermal growth f
35 65.5 16.2 1173 2 B97208 pyruvate ferredoxi
36 65 16.0 270 2 T27786 hypothetical prote
37 65 16.0 572 2 T29880 hypothetical prote
38 65 16.0 799 2 JC4126 integrin beta olig
39 65 16.0 915 2 B48225 probable proprotel
40 65 16.0 1342 2 A36223 kinase-related tra
41 65 16.0 3106 1 S53868 laminin alpha-2 ch
42 64.5 15.9 279 2 JG0164 LIM protein, FHL4
43 64.5 15.9 798 2 A28193 variant-specific s
44 64.5 15.9 3006 2 T28625 integrin beta-1 ch
45 64 15.8 97 2 S34769 eclosion hormone -

ALIGNMENTS

RESULT 1
T43251
furin (EC 3.4.21.75) - fall armyworm
N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43251
R;Cleplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A;Reference number: Z22368
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1299 <CIE>
A;Cross-references: EMBL:Z68888; NID:gl167859; PID:e219690, PIDN:CAA93116.1
A;Experimental source: clone sfurin 6; ovary
C;Function:
A;Description: responsible for the endoproteolytic processing of proproteins with specif
C;Keywords: hydrolase; serine proteinase

Query Match 20.1%; Score 81.5; DB 2; Length 1299;
Best Local Similarity 30.1%; Pred. No. 2.2; Indels 13; Gaps 3;
Matches 22; Conservative 5; Mismatches 33;

QY 1 CPBEQYWDPLGTCMSCKTICNHQSQTCAA----FCRKEQKGFYDHLRDICISCASIC 56
Db 1116 CLGSQYVDATSGTCRCDASC-----RTCSGPGQFCTCSRPLRIDRLANNQCVPCCSER 1170

QY 57 G-----QHPKQCAAY 65
Db 1171 GVTNSTPPTDCCH 1183

RESULT 2
H69834
hypothetical protein yhjQ - Bacillus subtilis

C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: H69834
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Broutillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Galler
Lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapicque, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauei
Y, M.; Oгава, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Poh, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Scoffone, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Author: Yoshikawa, H.F.; Zamestein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: H69834
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-108 <KUN>
 A:Cross-references: GB:299109; GB:AL009126; NID:G2633260; PIDN:CA812900.1; PID:ell83062;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yhjO

Query Match 19.8%; Score 80; DB 2; Length 108;
 Best Local Similarity 22.6%; Pred. No. 0.59;
 Matches 24; Conservative 7; Mismatches 25; Indels 50; Gaps 4;

QY 4 EOYMDLLGTCMSCKTICNH-----OSQRTCAFC----- 33
 DB 2 EGYSEACIACIDCMKACHCFTKCLSESVQHLSGCIPLDRCADICALAVKAMQTSBP 61
 QY 34 -----CRKEQGF-YDHLRDCISGASIGQHPRKOC 63
 DB 62 FKEKCALCADICEACGTGCGKHNDH---COACAKCFITCAEQC 103

RESULT 3
 T8626
 Variant-specific surface protein 2 - malaria parasite (*Plasmodium falciparum*)
 C:Species: *Plasmodium falciparum*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C:Accession: T28626
 R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guiney, F.; Herfel, J.A.; Peterson, D.S.
 Cell 82, 89-100, 1995
 A:Title: The large diverse gene family var encodes proteins involved in cytoadherence an
 A:Reference number: Z20487; MUID:95330813; PMID:7606788
 A:Accession: T28626
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2664 <SUX>
 A:Cross-references: EMBL:L40609; NID:G886376; PID:G886378; PIDN:AAA75398.1
 C:Genetics:
 A:Introns: 2197/3
 A:Note: var-2

Query Match 19.0%; Score 77; DB 2; Length 2664;
 Best Local Similarity 44.7%; Pred. No. 9.5;
 Matches 17; Conservative 4; Mismatches 9; Indels 8; Gaps 2;

QY 32 FCCRKEQGFYDHLRDCISGAS-----ICGQHPKOC 63
 DB 1031 FC-KEOSRLYELRLDCGSCCTGCKNNDKCAKCKOC 1066

RESULT 4
 S34583
 serine proteinase (EC 3.4.21.-) PC6B - mouse
 C:Species: *Mus musculus* (house mouse)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
 C:Accession: S34583
 R:Nakagawa, T.; Murakami, K.; Nakayama, K.
 FEBS Lett. 327, 165-171, 1993
 A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
 A:Reference number: S34583; MUID:93327934; PMID:8335106
 A:Accession: S34583
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1548 <NAK>
 A:Cross-references: GB:D17583; NID:G407344; PIDN:BA04507.1; PID:dl005033; PID:G440374
 C:Keywords: hydrolase, serine proteinase

Query Match 18.5%; Score 75; DB 2; Length 1548;
 Best Local Similarity 25.0%; Pred. No. 10;

Matches 21; Conservative 5; Mismatches 34; Indels 24; Gaps 3;
 QY 1 CPEBYMPDLGTCMSCKTICNHQS-----QRTCAFCCKRQGRKYPD 43
 DB 1152 CAAYVMBEGSHRCOPCKKCSRGSPSEDCYCTPRTFLNTTCVKEC---PEGHTD 1208

QY 44 HLRLDCISGASIC---GQHPKOC 63
 DB 1209 KDSQCIVLCHSSCRCTGCPHSMQC 1232

RESULT 5
 JC5571
 subtilisin-like proteinase convertase (EC 3.4.21.-) PACE4 precursor, splice form E-II -
 C:Species: *Homo sapiens* (man)
 C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
 C:Accession: JC5571
 R:Mori, K.; Kit, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; N
 J. Biochem. 121, 941-948, 1997
 A:Title: A novel human PACE4 isoform, PACE4E is an active processing protease containin
 A:Reference number: JC5570; MUID:97335942; PMID:9192737
 A:Accession: JC5571
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-962 <MR>
 A:Cross-references: DBJ:D87994; NID:G2330550; PIDN:BA021792.1; PID:G2330551
 A:Experimental source: brain cerebellum
 C:Comment: This enzyme is a processing protease and responsible for processing of vario
 ch it is retained intracellularly.
 C:Genetics:
 A:Gene: GDB:PACE4
 A:Cross-references: GDB:131390; OMIM:167405
 A:Map position: 15q26-15q26
 C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
 C:Keywords: glycoprotein; hydrolase; serine proteinase
 F1-62/Domain: signal sequence #status predicted <SIG>
 F1-62/Domain: propeptide #status predicted <PRO>
 F1-63-149/Domain: subtilisin homology <SBT>
 F1-96-954/Domain: hydrophobic cluster #status predicted <HCL>
 F1-96-954/Domain: hydrophobic cluster #status predicted
 F1-205-246,347,420/Active site: Asp, His, Ser #status predicted
 F1-259/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 74.5; DB 2; Length 962;
 Best Local Similarity 27.8%; Pred. No. 8.4;
 Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CMSCKT-ICNHQSRTCAFCCKRQGFYDHLRDCISC---ASIGQHPKOC 63
 DB 751 CUSCRGPFYHNDQMTCTVLC---PAGFYADESKNCKLKHPSCKKCYDEPKC 801

RESULT 6
 A39490
 subtilisin-like proteinase convertase (EC 3.4.21.-) PACE4 precursor, splice form A - hu
 N:Alternate names: Kexin homolog
 C:Species: *Homo sapiens* (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
 C:Accession: A39490
 R:Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J.
 DNA Cell Biol. 10, 757-769, 1991
 A:Title: Identification of a second human subtilisin-like protease gene in the fes/fps
 A:Reference number: A39490; MUID:92075167; PMID:1741956
 A:Accession: A39490
 A:Molecule type: mRNA
 A:Residues: 1-969 <KIB>
 A:Cross-references: GB:M80482; NID:G189531; PIDN:AAA59998.1; PID:G189532
 C:Genetics:
 A:Gene: GDB:PACE4
 A:Cross-references: GDB:131390; OMIM:167405
 A:Map position: 15q26-15q26
 C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
 C:Keywords: alternative splicing; hydrolase; serine proteinase
 F1-50-963/Product: serine proteinase PACE4 #status predicted <SIG>

F:196-434/Domain: subtilisin homology <SBT>
F:205,246,420/Active site: Asp, His, Ser #status predicted

Query Match 18.4%; Score 74.5; DB 1; Length 969;
Best Local Similarity 27.8%; Pred. No. 8.4;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CMCKT-ICNHQSORTCAAFCCRKEQKGYDHLRLDRCISC---ASICQHHPKC 63
DB 764 CLSCRRGFYHHQEMTCTVLC---PAGFYADESQKNCLKCHPSCKKCVDEPEKC 814

RESULT 7
JCS570
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-I - H
C:Species: Homo sapiens (man)
C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C:Accession: JCS570
R:Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, K.; Akamatsu, T.; Na
J. Biochem. 121, 941-948, 1997
A:Title: A novel human PACE4 isoform. PACE4E is an active processing protease containing
A:Reference number: JCS570; MUID:97335942; PMID:9192737
A:Accession: JCS570
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-975 <MOR>
A:CROSS-references: DBJ:D87993; NID:G2330548; PIDN:BAA21791.1; PID:G2330549
A:Experimental source: brain cerebellum
A:Comment: This enzyme is a processing protease and responsible for processing of various
ch it is retained intracellularly.
C:Genetics:
A:Gene: GDB:PACE4
A:CROSS-references: GDB:131390; OMIM:167405
A:Map position: 15q26-15q26
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: alternative splicing; glycoprotein; hydrolase; serine proteinase
F:1-62/Domain: signal sequence #status predicted <SIG>
F:63-149/Domain: propeptide #status predicted <PRO>
F:196-434/Domain: subtilisin homology <SBT>
F:952-968/Domain: hydrophobic cluster #status predicted <HCL>
F:205,246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F:259/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 74.5; DB 2; Length 975;
Best Local Similarity 27.8%; Pred. No. 8.4;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CMCKT-ICNHQSORTCAAFCCRKEQKGYDHLRLDRCISC---ASICQHHPKC 63
DB 764 CLSCRRGFYHHQEMTCTVLC---PAGFYADESQKNCLKCHPSCKKCVDEPEKC 814

RESULT 8
I46059
beta-1 integrin subunit - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
C:Accession: I46059
R:MacLaren, L.A.; Wildeman, A.G.
Biol. Reprod. 53, 153-165, 1995
A:Title: Fibronectin receptors in preimplantation development: cloning, expression, and
A:Reference number: I46059; MUID:95399478; PMID:7545439
A:Accession: I46059
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-773 <MAC>
A:CROSS-references: EMBL:U10865; NID:G520520; PIDN:AAA80571.1; PID:G520521
C:Superfamily: integrin beta chain; laminin-type EGF-like homology

Query Match 17.7%; Score 71.5; DB 2; Length 773;
Best Local Similarity 32.8%; Pred. No. 14;
Matches 21; Conservative 7; Mismatches 29; Indels 7; Gaps 4;

QY 8 DPLIGT--CMCK-TTICNHQSORTCAAFCCRKEQKGYDHLRLDRCISCASICQHHPK-Q 62
DB 568 DCSLIGTTCMAVNGQICNGRGVCECGA--CKTDPKFGQPTCEMCTCLGVCVAHKECVQ 625

QY 63 CAYF 66
DB 626 CRAP 629

RESULT 9
I52527
PACE4A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I52527
R:Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A:Title: PACE4A is a ubiquitous endoprotease that has similar but not identical substrates
A:Reference number: I52527
A:Accession: I52527
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-932 <RES>
A:CROSS-references: GB:D50060; NID:G769700; PIDN:BAA08777.1; PID:G769701
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F:172-410/Domain: subtilisin homology <SBT>

Query Match 17.7%; Score 71.5; DB 2; Length 932;
Best Local Similarity 29.6%; Pred. No. 16;
Matches 16; Conservative 7; Mismatches 24; Indels 7; Gaps 3;

QY 14 CMCKT-ICNHQSORTCAAFCCRKEQKGYDHLRLDRCISC---ASICQHHPKC 63
DB 727 CLSCRRGFYHHQEMTCTVLC---PAGFYADESQRLCHPSCKKCVDEPEKC 777

RESULT 10
A43434
furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Roelck, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.;
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:CROSS-references: GB:M94375; NID:G157461; PID:G157462
A:Note: sequence extracted from NCBI backbone (NCBI:111933, NCBI:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:CROSS-references: FlyBase:FBgn0004598
C:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 17.7%; Score 71.5; DB 2; Length 1680;
Best Local Similarity 32.1%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 23; Indels 9; Gaps 3;

QY 1 CPEBQYWDPLIGTTCMCKTICNHQSORTC---AACPCKEQKGY-DHLRLDRCISC 52
DB 1387 CLSSQYVDTTSATCKTC-----HDSCHSCRFPGQFCKGCVPLHLDLQLNSQCVSC 1437

RESULT 11
AD0715
conserved hypothetical protein STY1859 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar typhi

A>Note: this species has also been called *Salmonella typhi*
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C.Accession: A00715
R.Barthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Cronin, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mole, S.; O'Gaora, P.
Nature 413, 848-852, 2001.
A:Authors: Barry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov A:Reference number: A0502; PMID:1167608
A:Accession: A00715
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <PAR>
A:Cross-references: GB:AL51382; PIDN:CAD02093.1; PID:g16502928; GSPDB:GN00176
C:Genetics:
A:Gene: STY1859

Query Match 17.5%; Score 71; DB 2; Length 108;
Best Local Similarity 32.3%; Pred. No. 4.2;
Matches 21; Conservative 5; Mismatches 19; Indels 20; Gaps 5;

QY 3 EEOYWDPLGTGCMSCRTICNHGSGRTCAFCCKRKGKRYDHLRDCISGASICGQHPKQ 62
DB 59 EESYSGKL---CRLCADIC-----KCAECARHD---HDH---CONCARAC---SQ 98

QY 63 CAYFC 67
DB 99 CADAC 103

RESULT 12
158388
Protein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - human
C.Species: Homo sapiens (man)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C.Accession: I58388
R.Ziegler, S.F.; Bird, T.A.; Scherlinger, J.A.; Schooley, K.A.; Baum, P.R.
Oncogene 8, 663-670, 1993
A:Title: Molecular cloning and characterization of a novel receptor protein tyrosine kin A:Reference number: I58388; PMID:8382358
A:Accession: I58388
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1124 <RES>
A:Cross-references: GB:L06139; NID:g292823; PIDN:AAA61139.1; PID:g292824
C:Genetics:
A:Gene: GDB:TEK
A:Cross-references: GDB:344185; OMIM:600221
A:Map position: 9p21-9p21

A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: ATP autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho C:Keywords: ATP autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-1124/Product: protein-tyrosine kinase receptor type tek #status predicted <MAT>
F:135-137/Region: immunoglobulin homology <IM1>
F:135-137/Region: cell attachment (R-G-D) motif
F:211-251/Domain: EGF homology <EG1>
F:255-298/Domain: EGF homology <EG2>
F:302-340/Domain: EGF homology <EG3>
F:364-426/Domain: immunoglobulin homology <IM2>
F:447-527/Domain: fibronectin type III repeat homology <FN3A>
F:542-623/Domain: fibronectin type III repeat homology <FN3B>
F:638-720/Domain: fibronectin type III repeat homology <FN3C>
F:752-772/Domain: transmembrane #status predicted <TM>
F:822-1099/Domain: protein kinase #status predicted <KIN>
F:830-838/Region: protein kinase ATP-binding motif
F:140-158/Region: protein kinase ATP-binding site: carboxydrate (Asn) (covalent) #statu F:855,872,964/Active site: Lys, Glu, Asp #status predicted

Query Match 17.3%; Score 70; DB 1; Length 1124;
Best Local Similarity 26.4%; Pred. No. 25;

Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;
QY 3 EEOYDPP---LLGTCM-----SCRTIC-NHGSORTCAFCCKR 36
DB 212 EAKXKGPBENHLCSTACMNNGVCHEDTGECICPRGMRGTCEKACGLHFRGRTCKRCSGQ 271

QY 37 ECKGKYDHLRDCISGASICGQHPKQCAVFC 67
DB 272 ECKGKYVFCPLPYPGSCATGMKGLQCNAC 302

RESULT 13
S01659
Integrin beta-1 chain precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Aug-1999
C.Accession: S01659
R.Tominaga, S.I.
FEBS Lett. 238, 315-319, 1988
A:Title: Murine mRNA for the beta-subunit of integrin is increased in BALB/c-3T3 cells A:Reference number: S01659; PMID:89005707; PMID:3262537
A:Accession: S01659
A:Molecule type: mRNA
A:Residues: 1-798 <TOM>
A:Cross-references: EMBL:Y00769; NID:g52721; PIDN:CAA68738.1; PID:g52722
A>Note: the authors translated the codon ATT for residue 696 as Leu
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology
C:Keywords: cell adhesion; cytoskeleton; duplication; heterodimer; membrane protein F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-798/Product: integrin beta-1 chain #status predicted <MAT>

Query Match 17.2%; Score 69.5; DB 2; Length 798;
Best Local Similarity 29.3%; Pred. No. 22;
Matches 17; Conservative 8; Mismatches 28; Indels 5; Gaps 3;

QY 12 GTCMCK-TICNHGSGRTCAFCCKRKGKRYDHLRDCISGASICGQHPK--QCAVFC 66
DB 597 GPLASNGQICNGKICGCGA--CKTDPKFGPTCTCTGTCGACAHKEVCQRAIF 652

RESULT 14
IYMSFB
Fibronectin receptor beta chain precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C.Accession: P0104; B60597
R.Holers, V.M.; Ruff, T.G.; Parks, D.L.; McDonald, J.A.; Ballard, L.L.; Brown, E.J.
J. Exp. Med. 169, 1589-1605, 1989
A:Title: Molecular cloning of a murine fibronectin receptor and its expression during i for histocompatibility complex class II.
A:Reference number: P0104; PMID:89235580; PMID:2523953
A:Accession: P0104
A:Molecule type: mRNA
A:Residues: 1-799 <HOL>
A:Cross-references: GB:X15202; GB:Y00818; NID:g50986; PIDN:CAA33372.1; PID:g762977
A:Experimental source: strain BALB/c
A>Note: the DNA clones are missing the first nucleotide of Met-1
R.Rybeck, R.P.; McDonald, Bravo, H.; Zerial, M.; Bravo, R.
Exp. Cell Res. 180, 537-545, 1989
A:Title: Coordinate induction of fibronectin, fibronectin receptor, tropomyosin, and ac A:Reference number: B60597; PMID:89121031; PMID:2521606
A:Accession: B60597
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 596-799 <RYS>
C:Comment: The receptor is a heterodimer of alpha and beta chains.
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology
C:Keywords: cell adhesion; duplication; glycoprotein; heterodimer; receptor; transmembr F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-799/Product: fibronectin receptor beta chain #status predicted <MAT>
F:21-729/Domain: extracellular #status predicted <EXT>
F:730-752/Domain: transmembrane #status predicted <TRA>
F:753-799/Domain: intracellular #status predicted <INT>

F:50,94,97,212,269,363,406,417,482,521,585,670/Binding site: carbohydrate (Asn) (covalent)

Query Match 17.2%; Score 69.5; DB 1; Length 799;
 Best Local Similarity 29.3%; Pred. No. 22;
 Matches 17; Conservative 8; Mismatches 28; Indels 5; Gaps 3;
 QY 12 GTCMSCK-TICNHSQRTCAAFCCRKQKQFYDHLRLDCISCASICGQHPK--QCAIFY 66
 Db 598 GPCLASNGQICNGRIGCEGA--CKTDPKQSGPTCCTCTCLGVCAEHKEVCQCRAF 653

RESULT 15

G02428
 subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
 C:Accession: G02428
 R:Reudelhuber, T.L.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: H01242
 A:Accession: G02428
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-899 <REU>
 A:Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
 A:Gene: PCS
 C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
 C:Keywords: hydrolase; serine proteinase
 F:148-386/Domain: subtilisin homology <SBT>

Query Match 17.0%; Score 69; DB 2; Length 899;
 Best Local Similarity 26.0%; Pred. No. 27;
 Matches 19; Conservative 7; Mismatches 23; Indels 24; Gaps 5;

QY 1 CPBEQYWPDLGTCMSCKTICNHSQRTCAAF--C--CRK-----EQGKFYD 43
 Db 710 CPDGSYQDTKKNLCRKSENC-----KTCTEPHNTCTCRDGLSLQSGRCVSCEGRYFN 764
 QY 44 HLLRDCISCASIC 56
 Db 765 G--QDCQPCHRFC 775

Search completed: January 7, 2003, 09:41:19
 Job time : 10.5714 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 5.03759 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405

Sequence: 1 CPBEQYWDPLLTGTCMSCKTI.....DCISCASICGHPKQCAAYFC 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	97.0	293	T13X_HUMAN	O14836 homo sapien
2	256	63.2	249	T13X_MOUSE	O9et35 mus musculu
3	86.5	21.4	971	RECK_MOUSE	O92041 mus musculu
4	84.5	20.9	971	RECK_HUMAN	O95980 homo sapien
5	76.5	18.9	354	VEGD_HUMAN	O43915 homo sapien
6	76	18.8	297	XEDA_HUMAN	Q9hav5 homo sapien
7	75	18.5	1877	PK5_MOUSE	Q04592 mus musculu
8	74.5	18.4	969	PAC4_HUMAN	P29122 homo sapien
9	71.5	17.7	773	ITB1_BOVIN	P53712 bos taurus
10	71.5	17.7	1680	FUR2_DROME	P30432 drosophila
11	70	17.3	1124	TIE2_HUMAN	Q02763 homo sapien
12	69.5	17.2	798	ITB1_MOUSE	P09055 mus musculu
13	69	17.0	913	PK5_HUMAN	Q92824 homo sapien
14	68.5	16.9	501	TRAA_MOUSE	P39429 mus musculu
15	67.5	16.7	3084	LMA1_MOUSE	P19137 mus musculu
16	67	16.5	1210	EGFR_MOUSE	Q01279 mus musculu
17	67	16.5	3110	LMA2_HUMAN	P24043 homo sapien
18	66.5	16.4	184	TR17_HUMAN	Q02223 homo sapien
19	66.5	16.4	798	ITB1_FELCA	P53713 felis silve
20	66.5	16.4	937	PAC4_RAT	Q63415 rattus norv
21	66	16.3	60	MT_ICTPU	O93571 ictalurus p
22	66	16.3	1122	TIE2_MOUSE	Q02858 mus musculu
23	66	16.3	1210	EGFR_HUMAN	P00533 homo sapien
24	65.5	16.2	60	MT_GADMO	P51902 gadus morhu
25	65.5	16.2	358	VEGD_MOUSE	P97946 mus musculu
26	65.5	16.2	1426	EGFR_DROME	P04412 drosophila
27	65	16.0	739	ITB1_RAT	P49134 rattus norv
28	65	16.0	1339	ERB3_RAT	Q62799 rattus norv
29	65	16.0	1342	ERB3_HUMAN	P21860 homo sapien
30	65	16.0	1696	PK5_BRACL	Q9HJ15 branchiosto
31	65	16.0	1877	PK5_RAT	P41413 rattus norv
32	65	16.0	2569	LMA3_MOUSE	P61789 mus musculu
33	65	16.0	3106	LMA2_MOUSE	Q06075 mus musculu

34	64.5	15.9	443	1	FBL4_MOUSE	Q9evj9 mus musculu
35	64.5	15.9	798	1	ITB1_XENLA	P12606 xenopus lae
36	64	15.8	97	1	ECLH_DROME	Q07892 drosophila
37	64	15.8	119	1	ANTA_HAEGH	P16242 haementeria
38	64	15.8	1125	1	TIE2_BOVIN	Q06807 bos taurus
39	63.5	15.7	388	1	SH4_HUMAN	Q13839 homo sapien
40	63.5	15.7	400	1	LMB_HIRME	Q25092 hirudo medi
41	63.5	15.7	2482	1	VWF_PIG	Q28833 sus scrofa
42	63	15.6	474	1	TR1B_MOUSE	P25119 mus musculu
43	63	15.6	819	1	MTFC_HABIN	P71397 haemophilus
44	62.5	15.4	60	1	MTA_THERC	P52721 thermarces
45	62.5	15.4	388	1	SH4_CAVPO	O70528 cavia porce

ALIGNMENTS

RESULT 1
T13X_HUMAN
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC O14836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Straubeberg R.;
RX Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION
RX MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLYS";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating humoral immunity";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1 involved in the stimulation of B- and T-cell function and the regulation of humoral immunity.
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAML with its C-terminus.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting B-

cells and activated T-cells, but not in resting T-cells.
 CC - SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC - CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
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 CC -----
 CC EMBL; AF023614; AAC51790.1; -
 CC EMBL; BC028072; AAH28072.1; -
 CC Genew; HGNC:18153; TNFRSF13B.
 CC MIM; 604907; -
 CC InterPro; IPR001368; TNFR_C6.
 CC PROSITE; PS00652; TNFR_NGFR_1; 1.
 CC PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 CC Repeat.
 CC DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 187 293 TNFR-CYS 1.
 CC REPEAT 33 67 TNFR-CYS 2.
 CC DISULFID 70 104 BY SIMILARITY.
 CC DISULFID 34 47 BY SIMILARITY.
 CC DISULFID 50 62 BY SIMILARITY.
 CC DISULFID 71 86 BY SIMILARITY.
 CC DISULFID 89 100 BY SIMILARITY.
 CC DISULFID 93 104 BY SIMILARITY.
 CC CAROXYD 128 128 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FLICIT 251 251 P -> L (TN REF. 2).
 CC SEQUENCE 293 AA; 31816 MW; 411993F3DE17A5EB CRC64;
 CC
 CC Query Match 97.0%; Score 393; DB 1; Length 293;
 CC Best Local Similarity 94.4%; Pred. No. 66-34;
 CC Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 CC
 CC QY 1 CPEEQYWDPLGTGCMSCKTIQNHQSORTCAAF-CKRQCKFYDHLRLDCISCSASIC 56
 CC DB 34 CPEEQYWDPLGTGCMSCKTIQNHQSORTCAAFCRSLSCRKEQKPYDHLRLDCISCSASIC 93
 CC QY 57 GQHPKOCAYFC 67
 CC DB 94 GQHPKOCAYFC 104
 CC
 CC RESULT 2
 CC T13X MOUSE STANDARD; PRT; 249 AA.
 CC ID T13X MOUSE
 CC AC O9EBZ3; O9EBZ3; Rel. 41. Created
 CC DT 15-JUN-2002 (Rel. 41. Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41. Last annotation update)
 CC DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 CC activator and CAML interactor).
 CC GN TNFRSF13B OR TAC1.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 CC RX MEDLINE=2117254; PubMed=1081172;
 CC RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 CC Dixit V.M.;
 CC "Identification of a receptor for Blys demonstrates a crucial role in
 CC humoral immunity.";
 CC Nat. Immunol. 1:37-41 (2000).
 CC RT

[2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shimasawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito K., Okazaki Y., Gojobori T., Bono H., Kasuyama T., Saito K.,
 RA Kato K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann M., Gaasterland P., Glaser C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.W., Staubli F., Suzuki R., Tomita M., Wagner L., Watanabe T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
 RA Blake J., Botfield D., Boujard N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guastacchi S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 RN [3]
 RN FUNCTION.
 RP MEDLINE=20341628; PubMed=10860535;
 RX Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Heu H.;
 RA "TRAC1 is a TRAF-interacting receptor for TRAIL-1, a tumor necrosis
 RA factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:1137-1143 (2000).
 RN [4]
 RN FUNCTION.
 RP MEDLINE=21322748; PubMed=11429548;
 RX Wang H., Marsters S.A., Baker T., Chan B., Lee W.-P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RA "TRAC1-ligand interactions are required for T cell activation and
 RA collagen-induced arthritis in mice";
 RL Nat. Immunol. 2:632-637 (2001).
 CC - FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TAL1/BAFF/Blys
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC - SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLG with its C-terminus (by similarity).
 CC - SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC - SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -----
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 CC -----
 CC EMBL; AF257673; AAG00081.1; -
 CC EMBL; AF257673; BAB33457.1; -
 CC MGD; MGI:1889411; Tnfrsf13b.
 CC DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 CC DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 CC DOMAIN 1 128
 CC TRANSMEM 129 149
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 150 249
 CC REPEAT 5 38
 CC REPEAT 42 76
 CC TNFR-CYS 1.
 CC TNFR-CYS 2.


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CC -|- SUBUNIT: Interacts with MMP-9.
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -|- TISSUE SPECIFICITY: Expressed in various tissues and untransformed
CC cells. It is undetectable in tumor-derived cell lines and
CC oncogenically transformed cells.
CC -|- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; D50406; BAA34060.1; -.
DR EMBL; AL158830; CAD1384.1; -.
DR Genew; HGNC:11345; RECK.
DR MIM; 605227; -.
DR HSSP; P80424; IAN1.
DR InterPro; IPR002350; Kazal.
DR SMART; SM00280; KAZAL; 3.
DR SMART; SM00011; VWC def. 1.
DR PROSITE; PS00282; KAZAL; 1.
DR Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
DR Membrane; Anti-oncogene; Repeat.
DR SIGNAL 1 922
DR CHAIN 23 942
DR FT PROPEP 943 971
DR FT LIPID 942 942
DR FT DOMAIN 632 677
DR FT DOMAIN 708 750
DR FT DOMAIN 753 787
DR FT DOMAIN 37 338
DR FT REPEAT 37 84
DR FT REPEAT 104 141
DR FT REPEAT 151 197
DR FT REPEAT 216 263
DR FT REPEAT 292 338
DR FT DISULFID 633 654
DR FT DISULFID 633 658
DR FT DISULFID 643 677
DR FT CARBOHYD 39 633
DR FT CARBOHYD 86 666
DR FT CARBOHYD 200 200
DR FT CARBOHYD 297 297
DR FT CARBOHYD 352 352
DR FT SEQUENCE 971 AA; 106456 MW; 173D47D6AE6F834 CRC64;
DR Query Match 20.9%; Score 84.5; DB 1; Length 971;
DR Best Local Similarity 25.8%; Pred. No. 0.12; 27; Indels 35; Gaps 6;
DR Matches 25; Conservative 10; Mismatches 27;
DR QY 1 CPPE--QYWDPL-----IGTC-----MSCKTICNHSQRTCAFCCKRE 37
DR DB 74 CPEIWEIWNKNMNSLPGVFKSGDGVNGGCCCLALALECRQCKQASSKNDISKVCRS 133
DR QY 38 OGKPYDHLRLDCIS-----CASICGHPKQCAVFC 67
DR DB 134 ---YENALFSCISRNEMSGSVCCSYAGHH-TNCREVC 165
DR AC 043915;
DR DT 15-JUN-2002 (Rel. 41, Created)
DR DT 15-JUN-2002 (Rel. 41, Last sequence update)
DR DT 15-JUN-2002 (Rel. 41, Last annotation update)
DR DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DR growth factor) (FIGF).
DR GIGF OR VEGFD.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lung;
RX MEDLINE=97349118; PubMed=9205122;
RA Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Lung;
RX MEDLINE=98140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT between the FIGA and the GRP genes.";
RL Genomics 47:207-216(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818549; PubMed=9435229;
RA Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitrali A., Walks A.F.,
RA Altalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
RN [4]
RP PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX MEDLINE=20011413; PubMed=10542246;
RA Stacker S.A., Steiners K.L., Caesar C., Vitrali A., Domagala T.,
RA Nice E.C., Koufal S., Simpson R.J., Moritz R., Karpenen T.,
RA Altalo K., Achen M.G.;
RT "Biosynthesis of vascular endothelial growth factor-D involves
RT proteolytic processing which generates non-covalent homodimers.";
RL J. Biol. Chem. 274:32137-32136(1999).
RN [5]
RP FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
RN and endothelial cell growth, stimulating their proliferation and
RN migration and also has effects on the permeability of blood
RN vessels. May function in the formation of the venous and lymphatic
RN vascular systems during embryogenesis, and also in the maintenance
RN of differentiated lymphatic endothelium in adults. Binds and
RN activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
RN -|- SUBUNIT: Homodimer; non-covalent and antiparallel.
RN -|- SUBCELLULAR LOCATION: Secreted.
RN -|- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
RN intestine and fetal lung, and at lower levels in skeletal muscle,
RN colon, and pancreas.
RN -|- PTM: Undergoes a complex proteolytic maturation which generates a
RN variety of processed secreted forms with increased activity toward
RN VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
RN linked by disulfide bonds before secretion. The fully processed
RN VEGF-D is composed mostly of two VEGF homology domains (VHDS)
RN bound by non-covalent interactions.
RN -|- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
RN -----
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RN -----
DR EMBL; D89630; BAA24264.1; -.
DR EMBL; Y12863; CAA73370.1; -.
DR EMBL; Y12864; CAA73371.1; -.
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.

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RC STRAIN=ICR; TISSUE=Intestine; PubMed=8335106;
RX MEDLINE=93327934; PubMed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region of PCS, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
[2]
RP SEQUENCE FROM N.A. (ISOFORM PCSA).
RC TISSUE=Brain, and Intestine;
RX MEDLINE=93224489; PubMed=8468318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
NAkayama K.;
RT "Identification and functional expression of a new member of the mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4.";
RL J. Biochem. 113:132-135(1993).
[3]
RP SEQUENCE FROM N.A. (ISOFORM PCSA).
RC TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Jussion J., Vleau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a candidate proprotein convertase expressed in endocrine and nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
[4]
RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97103178; PubMed=8947550;
RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K., Bendayan M., Seidah N.G.;
RT "The isoforms of proprotein convertase PCS are sorted to different subcellular compartments.";
RL J. Cell Biol. 135:1261-1275(1996).
[5]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=86293359; PubMed=8638813;
RA Constant D.B., Calton M., Robertson E.J.;
RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
[6]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=97436919; PubMed=9291583;
RA Rancourt S.L., Rancourt D.E.;
RT "Mortine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
-1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION OF GROWTH FACTORS.
-1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
-1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO A PARACELLULAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES.
-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PCSB/LONG (SHOWN HERE) AND PCSA/SHORT. ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
-1- DEVELOPMENTAL STAGE: HEAVILY EXPRESSED THROUGHOUT THE EMBRYO, EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE KIDNEY AND THE LIVER, BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT E5.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DUCTAL AT E7.5, INTENSE EXPRESSION IN EXTRAMEMBRYONIC ENDODERM, ANIONIC AND NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK SAC FOLLOWED BY A CONFINANT EXPRESSION TO DERMAMYOTOME COMPARTMENT. BETWEEN E8.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL

CC	CELLS OF LIMB BUDS). AT EL2.5, EXPRESSION IN THE LIMBS IS CONFINED
CC	TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
CC	STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
CC	CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT EL6.5,
CC	ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
CC	ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
CC	ISOFORM B OCCUR AT EL2.5.
CC	-1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
CC	ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
CC	RETICULUM.
CC	-1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
CC	SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
CC	WITH THE TGN SORTING PROTEIN PALS-1.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
CC	-1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
CC	-----
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CC	-----
DR	EMBL; D17583; BAA04507.1; -
DR	EMBL; D12619; BAA02143.1; -
DR	EMBL; L14932; AAA74636.1; -
DR	PIR; JX0248; JX0248.
DR	PIR; A48225; A48225.
DR	HSSP; Q99405; 1MPT.
DR	MEROPS; S08.076; -
DR	MGD; MGI:97515; Pcsk5.
DR	InterPro; IPR000561; EGF-like.
DR	InterPro; IPR002174; Furin-like.
DR	InterPro; IPR002884; P domain.
DR	InterPro; IPR000209; Peptidase S8.
DR	Pfam; PF00082; Peptidase_S8; 1.
DR	Pfam; PF01483; P_PARTIAL
DR	PRINTS; PR00723; SUBTILISIN.
DR	PRODOM; PD000717; P domain; 1.
DR	SMART; SM00181; EGF_3.
DR	SMART; SM00001; EGF-like; 2.
DR	SMART; SM00261; FU; 22.
DR	PROSITE; PS00136; SUBTILASE_ASP; 1.
DR	PROSITE; PS00137; SUBTILASE_HIS; 1.
DR	PROSITE; PS00138; SUBTILASE_SBR; 1.
KW	Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
KW	Cleavage on pair of basic residues; Repeat; Alternating splicing;
KW	Transmembrane.
KW	SIGNAL
FT	1 34
FT	PROPEP
FT	35 1167
FT	CHAIN
FT	117 1877
FT	DOMAIN
FT	117 1768
FT	TRANSEM
FT	1769 1789
FT	DOMAIN
FT	1790 1877
FT	DOMAIN
FT	117 452
FT	DOMAIN
FT	464 602
FT	DOMAIN
FT	638 1753
FT	DOMAIN
FT	1825 1844
FT	DOMAIN
FT	1856 1877
FT	SITE
FT	116 117
FT	SITE
FT	521 523
FT	ACT_SITE
FT	173 173
FT	ACT_SITE
FT	214 214
FT	ACT_SITE
FT	388 388
FT	CARBOHYD
FT	227 227
FT	CARBOHYD
FT	383 383
FT	CARBOHYD
FT	667 667
FT	CARBOHYD
FT	754 754
FT	CARBOHYD
FT	804 804
FT	CARBOHYD
FT	854 854
FT	CARBOHYD
FT	951 951
FT	CARBOHYD

FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1220 1220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1711 1711 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1733 1733 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 878 915 GYIDQGHCHQTCCEASCAKMGPTQEDICISCPVTRVLD -->
FT ATEESWAEGGFCMLVKKNLCKQKVLQQLCKCTCTFQG
FT (IN ISOFORM PCSA).
FT VARSPLIC 916 1877 MISSING (IN ISOFORM PCSA).
SQ SEQUENCE 1877 AA; 209287 MW; EC850E2D20EA1C3 CRC64;

Query Match 18.5%; Score 75; DB 1; Length 1877;
Best Local Similarity 25.0%; Pred. No. 2;
Matches 21; Conservative 5; Mismatches 34; Indels 24; Gaps 3;

QY 1 CPBEQYWDPLLTGTCMCKTICNHQS-----QRTCAAPCCRKEQCKFYD 43
DB 1481 CAAYEYWDGSHRCQPCCHKKSCGFSBDCQCYTCPRFTPLNTTCVKEC---PEGYHTD 1537

QY 44 HLLRDCISASIC-----GOHPKQC 63
DB 1538 KDSQCVLCHSSCRTCEGPHSMQC 1561

RESULT 8
ID PAC4 HUMAN STANDARD; PRT; 969 AA.
AC P29122; Q15099; Q15100; Q9UEJ1; Q9UEJ2; Q9UEJ7; Q9UEJ8; Q9UEJ9;
AC Q9UEG7; Q9Y4G9; Q9Y4H0; Q9Y4H1;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
DE (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
DE convertase 4) (SPC4).
GN PAC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
RC TISSUE=Hepatosoma, and Kidney;
RX MEDLINE=92075167; PubMed=1741956;
RA Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
RA Bart P.J.;
RT Identification of a second human subtilisin-like protease gene in
RT the feg/fps region of chromosome 15.;
RL DNA Cell Biol. 10:757-769(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
RC TISSUE=Placenta;
RX MEDLINE=94235049; PubMed=8179631;
RA Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
RA Matsuda Y.;
RT Identification of novel cDNAs encoding human kexin-like protease,
RT PAC4 isoforms.;
RL Biochem. Biophys. Res. Commun. 200:943-950(1994).
RN [3]
RP ERRATUM.
RX MEDLINE=95071480; PubMed=7980617;
RA Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
RA Matsuda Y.;
RT Identification of novel cDNAs encoding human kexin-like protease,
RT PAC4 isoforms.;
RL Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
RC TISSUE=Placenta;
RA Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
RA Matsuda Y.;
RT Identification of a novel PAC4 isoform, PACE4E.;

Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
RC TISSUE=Cerebellum;
RX MEDLINE=9735942; PubMed=9192737;
RA Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
RA Akamatsu T., Nagamune H., Matsuda Y.;
RT "A novel human PAC4 isoform, PACE4E is an active processing protease
RT containing a hydrophobic cluster at the carboxy terminus.";
RL J. Biochem. 121:941-948(1997).
[6]
RP SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
RX MEDLINE=98021085; PubMed=9378725;
RA Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
RA Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.;
RT "Genomic organization and alternative splicing of human PACE4 (SPC4),
RT kexin-like processing endoprotease.";
RL J. Biochem. 122:438-452(1997).
[7]
RP ALTERNATIVE SPLICING (ISOFORM PACE4CS).
RX MEDLINE=97064242; PubMed=8906861;
RA Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.;
RT "Functional analysis of human PACE4-A and PACE4-C isoforms:
RT identification of a new PACE4-CS isoform.";
RL FEBS Lett. 396:31-36(1996).
[8]
RP CHARACTERIZATION.
RX MEDLINE=9233559; PubMed=10215603;
RA Sucic J.F., Moehring J.M., Innocencio N.M., Luchini J.W.,
RA Moehring T.J.;
RT "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and
RT can partly rescue the phenotype of a furin-deficient cell strain.";
RL Biochem. J. 339:639-647(1999).
[9]
RP PROCESSING.
RX MEDLINE=98408849; PubMed=9738469;
RA Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,
RA Tsuji A., Matsuda Y.;
RT "Biosynthetic processing and quaternary interactions of proprotein
RT convertase SPC4 (PACE4).";
RL FEBS Lett. 434:155-159(1998).
CC -!- FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTIDASE ACTIVITY WITHIN THE
CC CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
CC DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
CC AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
CC -!- CATALYTIC ACTIVITY. RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS,
CC WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC -!- COFACTOR: PACE4A IS PROBABLY CALCIUM-DEPENDENT.
CC -!- SUBUNIT: THE PACE4A-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE
CC RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
CC WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT
CC PROPEPTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.
CC -!- SUBCELLULAR LOCATION: PACE4A-I AND PACE4A-II ARE SECRETED. PACE4C
CC AND PACE4CS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM
CC IN ENDOPLASMIC RETICULUM. PACE4E-I AND PACE4E-II ARE RETAINED
CC INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
CC TERMINUS. PACE4B MIGHT BE SECRETED.
CC -!- ALTERNATIVE PRODUCTS: 8 ISOFORMS; PACE4A-I/PACE4 (SHOWN HERE),
CC PACE4A-II, PACE4B/PACE4.1, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
CC PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
CC C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
CC -!- TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
CC RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
CC PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS, BUT AT
CC COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
CC EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
CC KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
CC EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
CC PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
CC CEREBELLUM.
CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
CC ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC

RETICULUM. ISOFORM PAC64D LACKS THE PROPEPTIDE DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----

DR EMBL, M80482; AAA5998.1; -
DR EMBL, AB001914; BAA21620.1; -
DR EMBL, AB001898; BAA21620.1; JOINED.
DR EMBL, AB001900; BAA21620.1; JOINED.
DR EMBL, AB001901; BAA21620.1; JOINED.
DR EMBL, AB001902; BAA21620.1; JOINED.
DR EMBL, AB001903; BAA21620.1; JOINED.
DR EMBL, AB001904; BAA21620.1; JOINED.
DR EMBL, AB001905; BAA21620.1; JOINED.
DR EMBL, AB001914; BAA21621.1; -
DR EMBL, AB001898; BAA21621.1; JOINED.
DR EMBL, AB001900; BAA21621.1; JOINED.
DR EMBL, AB001901; BAA21621.1; JOINED.
DR EMBL, AB001902; BAA21621.1; JOINED.
DR EMBL, AB001903; BAA21621.1; JOINED.
DR EMBL, AB001904; BAA21621.1; JOINED.
DR EMBL, AB001905; BAA21621.1; JOINED.
DR EMBL, AB001906; BAA21621.1; JOINED.
DR EMBL, AB001907; BAA21621.1; JOINED.
DR EMBL, AB001908; BAA21621.1; JOINED.
DR EMBL, AB001909; BAA21621.1; JOINED.
DR EMBL, AB001914; BAA21622.1; -
DR EMBL, AB001901; BAA21622.1; JOINED.
DR EMBL, AB001902; BAA21622.1; JOINED.
DR EMBL, AB001903; BAA21622.1; JOINED.
DR EMBL, AB001904; BAA21622.1; JOINED.
DR EMBL, AB001905; BAA21622.1; JOINED.
DR EMBL, AB001906; BAA21622.1; JOINED.
DR EMBL, AB001907; BAA21622.1; JOINED.
DR EMBL, AB001908; BAA21622.1; JOINED.
DR EMBL, AB001909; BAA21622.1; JOINED.
DR EMBL, AB001914; BAA21623.1; -
DR EMBL, AB001898; BAA21623.1; JOINED.
DR EMBL, AB001900; BAA21623.1; JOINED.
DR EMBL, AB001901; BAA21623.1; JOINED.
DR EMBL, AB001902; BAA21623.1; JOINED.
DR EMBL, AB001903; BAA21623.1; JOINED.
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DR EMBL, AB001906; BAA21623.1; JOINED.
DR EMBL, AB001907; BAA21623.1; JOINED.
DR EMBL, AB001908; BAA21623.1; JOINED.
DR EMBL, AB001909; BAA21623.1; JOINED.
DR EMBL, AB001914; BAA21624.1; -
DR EMBL, AB001898; BAA21624.1; JOINED.
DR EMBL, AB001900; BAA21624.1; JOINED.
DR EMBL, AB001901; BAA21624.1; JOINED.
DR EMBL, AB001902; BAA21624.1; JOINED.
DR EMBL, AB001903; BAA21624.1; JOINED.
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DR EMBL, AB001905; BAA21624.1; JOINED.
DR EMBL, AB001906; BAA21624.1; JOINED.
DR EMBL, AB001907; BAA21624.1; JOINED.
DR EMBL, AB001908; BAA21624.1; JOINED.
DR EMBL, AB001909; BAA21624.1; JOINED.
DR EMBL, AB001914; BAA21625.1; -
DR EMBL, AB001898; BAA21625.1; JOINED.
DR EMBL, AB001900; BAA21625.1; JOINED.
DR EMBL, AB001901; BAA21625.1; JOINED.

DR EMBL, AB001902; BAA21625.1; JOINED.
DR EMBL, AB001903; BAA21625.1; JOINED.
DR EMBL, AB001904; BAA21625.1; JOINED.
DR EMBL, AB001905; BAA21625.1; JOINED.
DR EMBL, AB001906; BAA21625.1; JOINED.
DR EMBL, AB001907; BAA21625.1; JOINED.
DR EMBL, AB001908; BAA21625.1; JOINED.
DR EMBL, AB001909; BAA21625.1; JOINED.
DR EMBL, AB001910; BAA21625.1; JOINED.
Query Match 18.4%; Score 74.5; DB 1; Length 969;
Best Local Similarity 27.8%; Pred. No. 1.3;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;
Oy 14 CMSCKT-ICNHQSORTCAFCRKEOGKFYDHLRDCISC---ASICGHPKQC 63
Db 764 CLSCRGFHHQEMNTCVTLIC---PAGFYADESOKNCLKHPCKCKVDEPEKC 814
ID ITBL BOVIN STANDARD; PRT; 773 AA.
AC P53712;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Integrin beta-1 (Fibronectin receptor beta subunit) (CD29)
DE (Integrin VLA-4 beta subunit) (Fragment).
GN ITGB1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95399478; PubMed=7545439;
RA Maclaren L.A., Wildeman A.G.;
RT "Fibronectin receptors in preimplantation development: cloning,
RT expression, and localization of the alpha 5 and beta 1 integrin
RT subunits in bovine trophoblast.";
RL Biol. Reprod. 53:153-165(1995).
CC -1- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-
CC 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-
CC 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
CC SEQUENCE G-P-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-
CC 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
CC 10/BETA-1, ALPHA-11/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
CC THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRONECTIN.
CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
CC ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
CC FOR VCAM1 AND RECOGNIZES THE SEQUENCE A-E-I-D-S IN VCAM1. INTEGRIN
CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOACTIN AND
CC OSTEOPOINTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
CC CYTOACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPILGRIN
CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
CC WIDE ARRAY OF LIGANDS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
CC ALPHA-V.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORM BETA-1B
CC DOES NOT LOCALIZE TO FOCAL ADHESIONS.
CC -1- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
CC BONDS.
CC -1- SIMILARITY: CONTAINS 1 WFA-LIKE DOMAIN.
CC -----
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EMBL; U10865; AAA80571.1; -.
HSP; P05106; 1JUV2.
InterPro; IPR000561; EGF-like.
InterPro; IPR002369; Integrin_B.
InterPro; IPR001169; Integrin_beta_C.
InterPro; IPR003659; Plexin-like.
Pfam; PF00362; Integrin_B; 1.
ProDom; PD001811; Integrin_B; 1.
SMART; SM00001; EGF-like; 1.
SMART; SM00187; INB; 1.
SMART; SM00423; PSI; 1.
PROSITE; PS00243; INTEGRIN_BETA; 3.
PROSITE; PS00224; EGF_1; UNKNOWN 2.
Intergrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Repeat; Phosphorylation.
NON_TER 1
DOMAIN <1 705
TRANSMEM 706 728
DOMAIN 729 >773
DOMAIN 117 355
DOMAIN 443 612
REPEAT 443 492
REPEAT 493 536
REPEAT 537 575
REPEAT 576 612
DISULFID 4 441
DISULFID 12 22
DISULFID 15 52
DISULFID 25 41
DISULFID 184 190
DISULFID 238 278
DISULFID 378 392
DISULFID 412 668
DISULFID 439 443
DISULFID 454 466
DISULFID 463 502
DISULFID 468 477
DISULFID 479 493
DISULFID 508 513
DISULFID 510 545
DISULFID 515 530
DISULFID 532 537
DISULFID 551 556
DISULFID 553 584
DISULFID 558 567
DISULFID 569 576
DISULFID 590 595
DISULFID 592 638
DISULFID 597 607
DISULFID 610 613
DISULFID 617 626
DISULFID 623 700
DISULFID 642 766
MOD_RES 760 760
CARBOHYD 27 27
CARBOHYD 71 71
CARBOHYD 74 74
CARBOHYD 189 199
CARBOHYD 246 246
CARBOHYD 340 340
CARBOHYD 383 383
CARBOHYD 394 394
CARBOHYD 458 458
CARBOHYD 497 497
CARBOHYD 561 561
CARBOHYD 646 646
NON_TER 773 773
SEQUENCE 773 AA; 8532 MW; 5434086CE157195 CRC64;

Query Match 17.7%; Score 71.5; DB 1; Length 773;
Best Local Similarity 32.8%; Pred. No. 2.3; 29; Indels 7; Gaps 4;
Matches 21; Mismatches 7; Conservative 7; Indels 7; Gaps 4;
QY 8 DPLLGT-CMSCK-TICNHQSORTCAFCCKEQQKFDYDHLRLDCISASICGHPK-Q 62
DB 568 DCSLGTSTCMVANGQICNGRVCCEGA--CKTDFPQPTCEMCTCLGVCAEHKCVQ 625
QY 63 CAYF 66
DB 626 CRAF 629

RESULT 10

FUR2_DROME
ID FUR2_DROME STANDARD; PRT: 1680 AA.
AC P30432;
DT 01-APR-1993 (rel. 25, Created)
DT 01-APR-1993 (rel. 25, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
GN FUR2
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92381036; PubMed=1512259; Pauli I.G.L., Kurzik-Dumke U.,
RA Roebroek A.J.M., Creemers J.W.M., Leunissen J.A.F., van de Ven W.J.J.;
RA Rantrop M., Gateff E.A.F., expression of Dfurn2, a subtilisin-like
RT "Cloning and functional expression of Dfurn2, a subtilisin-like
RT proprotein processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
RT J. Biol. Chem. 267:17208-17215(1992).
CC -1- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTIDASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Release of mature proteins from their
CC propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
CC complement component C3 and von Willebrand factor from their
CC respective precursors.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
CC
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EMBL; M94375; AAA28551.1; -.
PIR; A43434; A43434.
HSSP; Q99405; IMPT.
MEROPS; S08.049; -.
Flybase; FBgn0004598; Fur2.
InterPro; IPR000561; EGF-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR002884; P domain.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PF01483; P; PARTIAL.
ProDom; PD00723; SUBTILISIN.
ProDom; PD000717; P domain; 1.
SMART; SM00181; EGF_1.
SMART; SM00261; FU; 10.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.

KM Hydroxylase; Serine protease; Glycoprotein; Signal; Transmembrane;
 KM Multigene family; Zymogen; Repeat.
 FT SIGNAL 1
 FT PROPEP 1
 FT CHAIN 320 1680
 FT ACT_SITE 418 418 FURIN-LIKE PROTEASE 2.
 FT ACT_SITE 457 457 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 638 638 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DOMAIN 962 1444 10 X TANDEM REPEATS, CYS-RICH.
 FT REPEAT 1006 1007 1.
 FT REPEAT 1008 1057 2.
 FT REPEAT 1058 1104 3.
 FT REPEAT 1105 1154 4.
 FT REPEAT 1154 1205 5.
 FT REPEAT 1206 1254 6.
 FT REPEAT 1255 1299 7.
 FT REPEAT 1300 1346 8.
 FT REPEAT 1347 1393 9.
 FT REPEAT 1394 1444 10.
 FT TRANSSEM 1508 1532 POTENTIAL.
 FT DOMAIN 1533 1680 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 928 928 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1061 1061 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1182 1182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1275 1275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1278 1278 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1440 1440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1680 AA; 183599 MW; 0A99CE8770A8E293 CRC64;
 Query Match 17.7%; Score 71.5; DB 1; Length 1680;
 Best Local Similarity 32.1%; Pred. No. 4.2;
 Matches 18; Conservative 6; Mismatches 23; Indels 9; Gaps 3;
 Qy 1 CPEQYDPLGLGTGMSCKTICNHSQRTG--AAFCCKEKGKEY-DHLRLDCISC 52
 Db 1387 CLSQGYDTTSATCKTC-----HDSCRSCFPGQFSCKGVPLHLQLNSQCVSC 1437
 RESULT 11
 TIE2 HUMAN STANDARD; PRT; 1124 AA.
 ID TIE2_HUMAN
 AC Q02763;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiopoietin 1 receptor precursor (BC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor TIR-2) (Tyrosine-protein kinase receptor TEK) (P140
 DE TEK) (Tunica interna endothelial cell kinase) (CD202b antigen).
 GN TEK OS TIE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=93173509; PubMed=8382358;
 RA Ziegler S.F., Bird T.A., Schreiner J.A., Schooley K.A., Baum P.R.;
 RT "Molecular cloning and characterization of a novel receptor protein
 RT tyrosine kinase from human placenta.";
 RL Oncogene 8:663-670(1993).
 RN [2]
 RP VARIANT VMCN1 TRP-849.
 RX MEDLINE=97134665; PubMed=8980225;
 RA Vukula M., Boon L.M., Caraway K.L. III, Calvert J.T., Diamonti A.J.,
 RA Goumurov B., Pasys K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
 RA Mulliken J.B., Olse B.R.;

RT "Vascular dysmorphogenesis caused by an activating mutation in the
 RT receptor tyrosine kinase TIE2.";
 RL Cell 87:1181-1190(1996).
 RN [3]
 RP VARIANTS VMCN1 TRP-849 AND SER-897.
 RX MEDLINE=9929243; PubMed=10369874;
 RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
 RA Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasys K.A.,
 RA Speer M.C., Peters K.G., Marchuk D.A.,
 RT "Allelic and locus heterogeneity in inherited venous malformations,"
 RL Hum. Mol. Genet. 8:1279-1289(1999).
 CC -1- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE KINASE TRANSMEMBRANE
 CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
 CC MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
 CC ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
 CC PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
 CC FORMATION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS
 CC AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
 CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
 CC ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
 CC -1- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
 CC MALFORMATIONS (VMCN1), AN ERROR OF VASCULAR MORPHOGENESIS
 CC CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TIE
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
 CC -1- DATABASE: NAME=PROV; NOTE=PROV 3.12-14(2002);
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1715848914_g.htm".
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: I06139; AAA61139.1; -
 CC HSSP: P1362; 1FGK.
 CC Genes: HGNC:11724; TEK.
 CC MIM: 600221; -
 CC MIM: 600195; -
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000719; Euk PKinase.
 CC InterPro: IPR003961; FN III.
 CC InterPro: IPR001245; Tyr PKinase.
 CC Pfam: PF00008; EGF_1;
 CC Pfam: PF00041; fn3_3;
 CC Pfam: PF00069; PKinase_1;
 CC PRINTS: PR00109; TYRKINASE.
 CC PRODOM: PD000001; Euk PKinase; 1.
 CC SMART: SM00181; EGF_2;
 CC SMART: SM00001; EGF-like; 1.
 CC SMART: SM00060; FN3_3;
 CC SMART: SM00219; Tyrc; 1.
 CC PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
 CC PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
 CC PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 CC PROSITE: PS00022; EGF_1; 3.
 CC PROSITE: PS01186; EGF_2; 3.
 CC Receptor; Tyrosine-protein kinase; Transmembrane; Immunoglobulin domain;
 CC Repeat; EGF-like domain; Transmembrane; Multigene family; Disease mutation;
 KM Glycoprotein; Phosphorylation; Signal; ATP-binding;
 FT CHAIN 19 1124
 FT DOMAIN 19 745
 FT TRANSSEM 746 770
 FT SIGNAL 18
 FT POTENTIAL.
 FT EXTRACELLULAR (POTENTIAL).

us-09-855-158-16.rsp

Tue Jan 7 10:36:54 2003

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FT DOMAIN 771 1124
FT DOMAIN 44 102
FT DOMAIN 210 252
FT DOMAIN 254 299
FT DOMAIN 301 341
FT DOMAIN 370 424
FT DOMAIN 444 536
FT DOMAIN 541 634
FT DOMAIN 638 732
FT DOMAIN 824 1096
FT NP_BIND 830 838
FT BINDING 855 855
FT ACT_SITE 964 964
FT CARBOHYD 140 140
FT CARBOHYD 158 158
FT CARBOHYD 339 339
FT CARBOHYD 438 438
FT CARBOHYD 464 464
FT CARBOHYD 560 560
FT CARBOHYD 596 596
FT CARBOHYD 649 649
FT CARBOHYD 691 691
FT MOD_RES 992 992
FT VARIANT 849 849
FT VARIANT 897 897
FT VARIANT 897 897
FT SEQUENCE 1124 AA; 125810 MW; 658C05D18FA4CCEC CRC64;

Query Match 17.3%; Score 70; DB 1; Length 1124;
Best Local Similarity 26.4%; Pred. No. 4.4;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;

QY 3 EBOYWDP-----LLGTCTN-----SCKTICN-HQSORTCAAFPCRK 36
Db 212 EAQKGFECNHLCTACNNGVCHDTGECICPFGMGRICERACELHTGRTCKERCSSQ 271
QY 37 EQGFYDHLRDCISACISGQHPKQCAVFC 67
Db 272 EGCKSVFCLPDPFGCCSACATGWKGLQCNAC 302

RESULT 12
ITBI_MOUSE STANDARD; PRT; 798 AA.
AC P09055;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Integrin beta-1 precursor (Fibronectin receptor beta subunit)
DE (CD29 antigen) (Integrin VLA-4 beta subunit).
GN ITGB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=89005707; PubMed=3262537;
RA Tomimaga S.;
RT "Murine mRNA for the beta-subunit of integrin is increased in
RT BALB/c-3T3 cells entering the G1 phase from the G0 state.";
RL FEBS Lett. 238:315-319(1988).
RN [2]
RP SEQUENCE OF 2-798 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=89235580; PubMed=2523953;
RA Holers V.M.; Ruff T.G.; Parks D.L.; McDonald J.A.; Ballard L.L.;
RA Brown E.J.;
RT "Molecular cloning of a murine fibronectin receptor and its
RT expression during inflammation. Expression of VLA-5 is increased in
RT activated peritoneal macrophages in a manner discordant from major

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histocompatibility complex class II.";
J. Exp. Med. 169:1589-1605(1989).
-1- FUNCTION. INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-1
1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-
1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
SEQUENCE G-P-G-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-
3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
FOR VCAM1 AND RECOGNIZES THE SEQUENCE O-I-D-S IN VCAM1. INTEGRIN
ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND
CYTOSPONTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPILIGRIN
AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
WIDE ARRAY OF LIGANDS.
-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
ALPHA-V.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE INTEGRIN BETA FAMILY.
-1- SIMILARITY: CONTAINS 1 VMPA-LIKE DOMAIN.
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EMBL; Y00769; CAA68738.1; -;
EMBL; X15202; CAA33272.1; -;
PIR; F01004; IJMSPB.
PIR; S01659; S01659.
HSSP; P05106; IJVB2.
MGI; I96610; Itgb1.
InterPro; IPR000561; EGF-like.
InterPro; IPR002369; Integrin_B.
InterPro; IPR001169; Integrin_beta_C.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002035; VWF_A.
Pfam; PF00362; Integrin_B_1.
PRINTS; PR01186; INTEGRINB.
ProDom; PD001811; Integrin_B_1.
SMART; SM00001; EGF_like; 1.
SMART; SM00187; INB; 1.
SMART; SM00423; PSI; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS00243; INTEGRIN_BETA; 3.
PROSITE; PS00022; EGF_1; UNKNOWN 2.
Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
Repeat; Signal; Phosphorylation.
SIGNAL 1 20
CHAIN 21 798
DOMAIN 21 728 INTEGRIN BETA-1.
DOMAIN 729 751 EXTRACELLULAR (POTENTIAL).
DOMAIN 752 798 POTENTIAL.
DOMAIN 140 378 CYTOPLASMIC (POTENTIAL).
DOMAIN 466 635 VMPA-LIKE.
DOMAIN 466 515 4 CYSTEINE-RICH TANDEM REPEATS.
REPEAT 466 515 I.
REPEAT 516 559 II.
REPEAT 560 598 III.
REPEAT 599 635 IV.
DISULFID 27 464 BY SIMILARITY.
DISULFID 35 45 BY SIMILARITY.
DISULFID 48 75 BY SIMILARITY.
DISULFID 38 64 BY SIMILARITY.

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Query Match

Best Local Similarity 17.2%; Score 69.5; DB 1; Length 798;

Matches 17; Conservative 8; Mismatches 28; Indels 5; Gaps

Db 597 gpcLANSNGOICNGRGICEGGA--CKCTDPKFGGPTCTCTGTCGLGCAEHKRCVGCRAAF 652

12 GTGMSCK-TTICNHSORTCAAFCCREKQGFYDLHLRDCISCAISICGHPK--QCAVF 66

1:1

PKCS_HUMAN STANDARD; PRT; 913 AA.

RESULT 13

PKCS_HUMAN

ID PKCS_HUMAN STANDARD; PRT; 913 AA.

1:1

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)

(proprotein convertase PCS) (Subtilisin/kexin-like protease PCS)

(convertase PCS) (PC6) (hpc6).

DE

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

1:1

SEQUENCE FROM N.A.

TISSUE=Testis;

MDL=96353880; PubMed=8755538;

Miranda L., Wolf J., Pichuanes S., Duke R., Franzoso A.;

"Isolation of the human PC6 gene encoding the putative host protease

for HIV-1 gp160 processing in CD4⁺ lymphocytes.";

FT DISULFID 207 213 BY SIMILARITY.

FT DISULFID 261 301 BY SIMILARITY.

FT DISULFID 401 415 BY SIMILARITY.

FT DISULFID 435 691 BY SIMILARITY.

FT DISULFID 462 477 BY SIMILARITY.

FT DISULFID 477 489 BY SIMILARITY.

FT DISULFID 486 525 BY SIMILARITY.

FT DISULFID 491 520 BY SIMILARITY.

FT DISULFID 502 336 BY SIMILARITY.

FT DISULFID 531 358 BY SIMILARITY.

FT DISULFID 533 353 BY SIMILARITY.

FT DISULFID 538 553 BY SIMILARITY.

FT DISULFID 555 560 BY SIMILARITY.

FT DISULFID 574 579 BY SIMILARITY.

FT DISULFID 576 607 BY SIMILARITY.

FT DISULFID 581 590 BY SIMILARITY.

FT DISULFID 592 599 BY SIMILARITY.

FT DISULFID 613 618 BY SIMILARITY.

FT DISULFID 615 661 BY SIMILARITY.

FT DISULFID 620 630 BY SIMILARITY.

FT DISULFID 633 636 BY SIMILARITY.

FT DISULFID 640 649 BY SIMILARITY.

FT DISULFID 646 723 BY SIMILARITY.

FT DISULFID 665 699 BY SIMILARITY.

FT MOD RES 783 783 BY SIMILARITY.

FT CARBOHYD 50 50 PHOSPHORYLATION (BY SIMILARITY).

FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 564 584 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 659 659 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 385 385 E -> P (IN REF. 2).

FT CONFLICT 392 392 G -> A (IN REF. 2).

FT CONFLICT 443 445 IRT1 HSK1 (IN REF. 2).

FT SEQUENCE 798 AA; 88231 MW; 26785F70A168B56 CRC64;

```

FT CONFLICT 601 601 R -> O (IN REF. 3).
SQ SEQUENCE 913 AA; 101775 MW; 21389264CAD7546C CRC64;
Query Match 17.0%; Score 69; DB 1; Length 913;
Best Local Similarity 26.0%; Pred. No. 4.7;
Matches 19; Conservative 7; Mismatches 23; Indels 24; Gaps 5;

QY 1 CPEQYWDPLGTCMSCKTICNHOSQRTCAAF--C--CRK-----EQKFPYD 43
Db 724 CPDGSQDTKKNLCRKCSENC-----KTCTEPHCTECRDGLSLGSRCSVSCEDGRYFN 778
QY 44 HLRDPCISCASIC 56
Db 779 G--QDCPCHRFC 789

RESULT 14
TRA2_MOUSE
ID TRA2_MOUSE STANDARD; PRT; 501 AA.
AC P19429;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE TNF receptor associated factor 2 (TNFR2).
GN TNF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349371; PubMed=8069916;
RA Roche M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor."
RL Cell 78:681-692(1994).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
CC ACTIVATES NF-KAPPA-B.
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
CC HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
CC FACTORS 1 AND 2 (IAPs) TO RECRUIT THEM TO THE TUMOR NECROSIS
CC FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
CC -----
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CC -----
DR EMBL; L35303; AAC37662.1; -
DR HSSP; L12351; IHWT.
DR MGD; MGI:101835; Traf2.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR001007; TRAF.
DR InterPro; IPR001293; Znf_TRAF.
DR InterPro; IPR001841; Znf_Ting.
DR Pfam; PF00097; ZF-C3HC4_1.
DR Pfam; PF00917; MATH_1.
DR Pfam; PF02167; ZF-TRAF_2.
DR SMART; SM00161; MATH; 1.
DR SMART; SM00161; TRAF; 1.
DR SMART; SM00161; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00518; ZF_RING_2; 1.
DR PROSITE; PS00518; ZF_RING_3; 1.
DR PROSITE; PS00518; ZF_RING_4; 1.
DR PROSITE; PS00518; ZF_RING_5; 1.
DR PROSITE; PS00518; ZF_RING_6; 1.
DR PROSITE; PS00518; ZF_RING_7; 1.
DR PROSITE; PS00518; ZF_RING_8; 1.
DR PROSITE; PS00518; ZF_RING_9; 1.
DR PROSITE; PS00518; ZF_RING_10; 1.
DR PROSITE; PS00518; ZF_RING_11; 1.
DR PROSITE; PS00518; ZF_RING_12; 1.
DR PROSITE; PS00518; ZF_RING_13; 1.
DR PROSITE; PS00518; ZF_RING_14; 1.
DR PROSITE; PS00518; ZF_RING_15; 1.
DR PROSITE; PS00518; ZF_RING_16; 1.
DR PROSITE; PS00518; ZF_RING_17; 1.
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DR PROSITE; PS00518; ZF_RING_21; 1.
DR PROSITE; PS00518; ZF_RING_22; 1.
DR PROSITE; PS00518; ZF_RING_23; 1.
DR PROSITE; PS00518; ZF_RING_24; 1.
DR PROSITE; PS00518; ZF_RING_25; 1.
DR PROSITE; PS00518; ZF_RING_26; 1.
DR PROSITE; PS00518; ZF_RING_27; 1.
DR PROSITE; PS00518; ZF_RING_28; 1.
DR PROSITE; PS00518; ZF_RING_29; 1.
DR PROSITE; PS00518; ZF_RING_30; 1.
DR PROSITE; PS00518; ZF_RING_31; 1.
DR PROSITE; PS00518; ZF_RING_32; 1.
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DR PROSITE; PS00518; ZF_RING_34; 1.
DR PROSITE; PS00518; ZF_RING_35; 1.
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DR PROSITE; PS00518; ZF_RING_37; 1.
DR PROSITE; PS00518; ZF_RING_38; 1.
DR PROSITE; PS00518; ZF_RING_39; 1.
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DR PROSITE; PS00518; ZF_RING_41; 1.
DR PROSITE; PS00518; ZF_RING_42; 1.
DR PROSITE; PS00518; ZF_RING_43; 1.
DR PROSITE; PS00518; ZF_RING_44; 1.
DR PROSITE; PS00518; ZF_RING_45; 1.
DR PROSITE; PS00518; ZF_RING_46; 1.
DR PROSITE; PS00518; ZF_RING_47; 1.
DR PROSITE; PS00518; ZF_RING_48; 1.
DR PROSITE; PS00518; ZF_RING_49; 1.
DR PROSITE; PS00518; ZF_RING_50; 1.
DR PROSITE; PS00518; ZF_RING_51; 1.
DR PROSITE; PS00518; ZF_RING_52; 1.
DR PROSITE; PS00518; ZF_RING_53; 1.
DR PROSITE; PS00518; ZF_RING_54; 1.
DR PROSITE; PS00518; ZF_RING_55; 1.
DR PROSITE; PS00518; ZF_RING_56; 1.
DR PROSITE; PS00518; ZF_RING_57; 1.
DR PROSITE; PS00518; ZF_RING_58; 1.
DR PROSITE; PS00518; ZF_RING_59; 1.
DR PROSITE; PS00518; ZF_RING_60; 1.
DR PROSITE; PS00518; ZF_RING_61; 1.
DR PROSITE; PS00518; ZF_RING_62; 1.
DR PROSITE; PS00518; ZF_RING_63; 1.
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DR PROSITE; PS00518; ZF_RING_454; 1.
DR PROSITE; PS00518; ZF_RING_455; 1.
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DR PROSITE; PS00518; ZF_RING_457; 1.
DR PROSITE; PS00518; ZF_RING_458; 1.
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DR PROSITE; PS00518; ZF_RING_460; 1.
DR PROSITE; PS00518; ZF_RING_461; 1.
DR PROSITE; PS00518; ZF_RING_462; 1.
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DR PROSITE; PS00518; ZF_RING_472; 1.
DR PROSITE; PS00518; ZF_RING_473; 1.
DR PROSITE; PS00518; ZF_RING_474; 1.
DR PROSITE; PS00518; ZF_RING_475; 1.
DR PROSITE; PS00518; ZF_RING_476; 1.
DR PROSITE; PS00518; ZF_RING_477; 1.
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DR PROSITE; PS00518; ZF_RING_479; 1.
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DR PROSITE; PS00518; ZF_RING_481; 1.
DR PROSITE; PS00518; ZF_RING_482; 1.
DR PROSITE; PS00518; ZF_RING_483; 1.
DR PROSITE; PS00518; ZF_RING_484; 1.
DR PROSITE; PS00518; ZF_RING
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CC -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; J04064; AAA39410.1; --
DR EMBL; X07737; CAA30561.1; --
DR EMBL; X13459; CAA31807.1; --
DR EMBL; M36775; AAA39406.1; --
DR PIR; A31771; MMMSA.
DR HSP; Q60675; IQUO.
DR MGD; MGI:99892; Lamal.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001896; LamNT.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00052; laminin_B; 2.
DR Pfam; PF00053; laminin_EGF; 15.
DR Pfam; PF00054; laminin_G; 5.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD002082; LamNT; 1.
DR ProDom; PD003031; Laminin_B; 2.
DR SMART; SM00180; EGF_Lam; 14.
DR SMART; SM00281; LamB; 2.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 15.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR Glycoprotein; Basenent membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 25 3084
FT MOD_RES 25 25
FT DOMAIN 25 276 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 277 333 LAMININ EGF-LIKE 1.
FT DOMAIN 334 403 LAMININ EGF-LIKE 2.
FT DOMAIN 404 460 LAMININ EGF-LIKE 3.
FT DOMAIN 461 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 519 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 520 715 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 716 748 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 749 797 LAMININ EGF-LIKE 6.
FT DOMAIN 798 855 LAMININ EGF-LIKE 7.
FT DOMAIN 856 908 LAMININ EGF-LIKE 8.
FT DOMAIN 909 957 LAMININ EGF-LIKE 9.
FT DOMAIN 958 1004 LAMININ EGF-LIKE 10.
FT DOMAIN 1005 1050 LAMININ EGF-LIKE 11.
FT DOMAIN 1051 1096 LAMININ EGF-LIKE 12.
FT DOMAIN 1097 1156 LAMININ EGF-LIKE 13.
FT DOMAIN 1157 1166 LAMININ EGF-LIKE 14 (N-TERMINAL).
FT DOMAIN 1167 1368 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1369 1409 LAMININ EGF-LIKE 14 (C-TERMINAL).
FT DOMAIN 1410 1458 LAMININ EGF-LIKE 15.
FT DOMAIN 1459 1515 LAMININ EGF-LIKE 16.
FT DOMAIN 1516 1562 LAMININ EGF-LIKE 17.
FT DOMAIN 1564 2124 DOMAIN II AND I.
FT DOMAIN 2125 2305 LAMININ G-LIKE 1.
FT DOMAIN 2313 2489 LAMININ G-LIKE 2.
FT DOMAIN 2494 2680 LAMININ G-LIKE 3.
FT DOMAIN 2722 2894 LAMININ G-LIKE 4.
FT DOMAIN 2899 3079 LAMININ G-LIKE 5.
FT DOMAIN 1612 1820 COILED COIL (POTENTIAL).
FT DOMAIN 1869 1903 COILED COIL (POTENTIAL).

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FT DOMAIN 2096 2128 COILED COIL (POTENTIAL).
FT SITE 1147 CELL ATTACHMENT SITE.
FT DISULFID 227 BY SIMILARITY.
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FT DISULFID 1412 BY SIMILARITY.
FT DISULFID 1429 BY SIMILARITY.
FT DISULFID 1441 BY SIMILARITY.
FT DISULFID 1459 BY SIMILARITY.
FT DISULFID 1461 BY SIMILARITY.
FT DISULFID 1486 BY SIMILARITY.
FT DISULFID 1498 BY SIMILARITY.
FT DISULFID 1516 BY SIMILARITY.
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FT DISULFID 1537 BY SIMILARITY.
FT DISULFID 1549 BY SIMILARITY.
FT DISULFID 1563 BY SIMILARITY.
FT DISULFID 1567 BY SIMILARITY.
FT CARBOHYD 45 45 INTERCHAIN (PROBABLE).
FT CARBOHYD 79 79 INTERCHAIN (PROBABLE).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 770 770 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 857 857 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 914 914 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 959 959 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 969 969 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1052 1052 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 1344 1344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1414 1414 N-LINKED (GLCNAC. . .) (POTENTIAL).
Query Match 16.7%; Score 67.5; DB 1; Length 3084;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 19; Conservative 4; Mismatches 17; Indels 17; Gaps 4;
QY 9 PLAGTCMCKTICNHSQRTCAAFCCCKEKGKFDHLDKISCAS-ICQHPKQCA 64
DB 1402 PILAPCVPCN--CNNHSD-----VCDPRTGK-----CUSCRDHTSGDHCELC 1442

Search completed: January 7, 2003, 09:38:12
JOB time : 6.03759 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 18.9749 seconds
(Without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-16
Perfect score: 405
Sequence: 1 CPEQYWDPLIGTMSCKT.....DCISCASICGHPKQCAVFC 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: SPREMBL_21:
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81.5	20.1	1299	5 Q26489	Q26489 spodoptera
2	80	19.8	108	5 C07571	C07571 bacillus su
3	77	19.0	2664	5 Q26033	Q26033 plasmodium
4	76.5	18.9	783	5 P92163	P92163 stromyloce
5	75.5	18.6	704	3 Q74567	Q74567 trichodema
6	75	18.5	1069	5 Q9BPS2	Q9BPS2 bombyx mori
7	74	18.3	723	11 Q9D2H5	Q9D2H5 mus musculu
8	71.5	17.7	213	11 Q9LE4	Q9LE4 mus musculu
9	71.5	17.7	214	11 Q8ROY1	Q8ROY1 mus musculu
10	71.5	17.7	296	11 Q35171	Q35171 mus musculu
11	71.5	17.7	932	11 Q62030	Q62030 mus musculu
12	71.5	17.7	1376	5 Q8S2S2	Q8S2S2 drosophila
13	71.5	17.7	1679	5 Q24301	Q24301 drosophila
14	71	17.5	108	16 Q8ZPY1	Q8ZPY1 salmonella
15	71	17.5	108	16 Q8ZC68	Q8ZC68 salmonella
16	71	17.5	210	4 Q9BYR0	Q9BYR0 homo sapien

17	71	17.5	761	6 Q9SLQ2	Q9SLQ2 macaca fasc
18	71	17.5	1023	4 Q9UL17	Q9UL17 homo sapien
19	71	17.5	1704	5 Q94446	Q94446 chironomus
20	70.5	17.4	1362	13 Q9PV24	Q9PV24 xenopus lae
21	70	17.3	598	11 Q8RI51	Q8RI51 mus musculu
22	70	17.3	1557	5 Q8WPK9	Q8WPK9 olkopleura
23	69.5	17.2	98	5 Q16939	Q16939 ancylostoma
24	69.5	17.2	109	2 Q68643	Q68643 pseudomonas
25	69.5	17.2	166	4 Q9BYR3	Q9BYR3 homo sapien
26	69.5	17.2	271	5 Q9VU12	Q9VU12 drosophila
27	69	17.0	154	4 Q9BYP9	Q9BYP9 homo sapien
28	69	17.0	913	4 Q9SEP4	Q9SEP4 homo sapien
29	69	17.0	1137	4 Q9H8C1	Q9H8C1 homo sapien
30	69	17.0	1918	4 Q9BOM7	Q9BOM7 homo sapien
31	69	17.0	1925	4 Q9P2E3	Q9P2E3 homo sapien
32	68.5	16.9	1438	11 Q922M5	Q922M5 mus musculu
33	68.5	16.9	508	11 Q54896	Q54896 mus musculu
34	68	16.8	433	11 Q91ZM5	Q91ZM5 ratius norv
35	67.5	16.7	146	10 Q40579	Q40579 nicotiana t
36	67.5	16.7	777	10 Q9LU38	Q9LU38 arabidopsis
37	67.5	16.7	798	5 Q8SQC0	Q8SQC0 bos taurus
38	67.5	16.7	2232	5 Q94711	Q94711 paramacium
39	67	16.5	136	11 Q99PK1	Q99PK1 mus musculu
40	67	16.5	643	11 Q9ERVE	Q9ERVE mus musculu
41	67	16.5	655	11 Q9WV75	Q9WV75 mus musculu
42	67	16.5	1083	11 Q9QW24	Q9QW24 ratius sp.
43	67	16.5	1210	11 Q9EP98	Q9EP98 mus musculu
44	67	16.5	2108	13 Q98019	Q98019 gallus gall
45	66.5	16.4	133	16 Q8XS26	Q8XS26 ralsstonia s

ALIGNMENTS

RESULT 1
ID Q26489 PRELIMINARY; PRT; 1299 AA.

AC Q26489; 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Endoprotease furin.
GN FURIN
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pierisidae; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
CC Noctuidae; Noctuidae; Amphipyriinae; Spodoptera.
CX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RF TISSUE=SF9; Klenk H.;
RA "Cloning and functional characterization of FURIN from Spodoptera
RT frugiperda (SF9) cells."
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68888; CAA9316.1; -.
DR HSSP; Q99405; 1PRT; Furin-like
DR InterPro; IPR002174; Furin-like
DR InterPro; IPR002099; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR Pfam; PF01483; P_1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.

SO SEQUENCE. 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;
Query Match 20.1%; Score 81.5; DB 5; Length 1299;
Best Local Similarity 30.1%; Pred. No. 0.038;

Matches 22; Conservative 5; Mismatches 33; Indels 13; Gaps 3;

QY 1 CPBQWDPPLGTCMCKTICNHQSORTCAA-----FCRKEQKGYDHLRLDCISCSASIC 56
 Db 1116 CLGQYDATSGFRCSDASC-----RTCSGQFSCTTCRPLRLDRLNQCVPCCSER 1170
 QY 57 G-----QHPKQAY 65
 Db 1171 GVTNTPPTDCCH 1183

RESULT 2

ID O07571 PRELIMINARY; PRT; 108 AA.
 AC O07571;
 DT 01-JUL-1997 (TREMELrel. 04, Created)
 DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE Hypothetical protein ynjQ.
 GN ynjQ.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 [1] _____
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RC Noback M.A., Terptrata P., Holsappel S., Venema G., Bron S.;
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 [2] _____
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RC MEDLINE=98044013; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Borriello R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Enrioz F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D., N.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Glim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grand G.,
 Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Rieger M., Rivolta C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terptrata P., Tognoni A.,
 Tostato V., Uchiyama S., Vandenbol M., Vannier P., Vassatotti A.,
 Winters P., Wipat K., Wedler H., Wedler H., Weltenecker F., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Banchin A.;
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256 (1997).
 RN [1] _____
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Banchin A.;
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL; Y14081; CAA74479.1; -;
 DR EMBL; Z99109; CAB12900.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 108 AA; 11839 MW; 78637689ABB0FD8F CRC64;

Query Match 19.8%; Score 80; DB 16; Length 108;
 Best Local Similarity 22.6%; Pred. No. 0.006;
 Matches 24; Conservative 7; Mismatches 25; Indels 50; Gaps 4;
 QY 4 EYWDPLGLTCSCKTICNH-----QSORTCAAF----- 33
 Db 2 EYSEACIEACIDCKACNHCFTKLEESVQHLSGCGIRLDRECDICALAVKAMQTDSP 61
 QY 34 -----CRKEQKGF-YDHLRLDCISCSASICGQHPKQC 63
 Db 62 FMKEICALCADICEACGTECGKHIDH-----CQACAKACFTCAEQC 103

RESULT 3

ID Q26033 PRELIMINARY; PRT; 2664 AA.
 AC Q26033;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Variant-specific surface protein.
 GN VAR-2.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 [1] _____
 RN SEQUENCE FROM N.A.
 RP STRAIN=FCR3;
 RC MEDLINE=95330813; PubMed=7606788;
 RA Su X.Z., Heatwole V.M., Wertheimer S.P., Guinet P., Herrfeldt J.A.,
 Peterson D.S., Ravetch J.A., Wellem T.E.;
 RT "The large diverse gene family var encodes proteins involved in
 cytoadherence and antigenic variation of Plasmodium falciparum-
 RT infected erythrocytes.";
 RL Cell 82:89-100 (1995).
 DR EMBL; L40609; AAA75398.1; -;
 DR InterPro; IPR004258; PREMP.
 DR Pfam; PF03011; PREMP; 2
 SQ SEQUENCE 2664 AA; 302410 MW; 6EA2468511703091 CRC64;

Query Match 19.0%; Score 77; DB 5; Length 2664;
 Best Local Similarity 44.7%; Pred. No. 0.28;
 Matches 17; Conservative 4; Mismatches 9; Indels 8; Gaps 2;

QY 32 FCRKEQKGYDHLRLDCISCS-----ICGQHPKQC 63
 Db 1031 FC--REQSRLYEELRLDCGCTTGKCNNDKCAKCDKQC 1066

RESULT 4

ID P92163 PRELIMINARY; PRT; 783 AA.
 AC P92163;
 DT 01-MAY-1997 (TREMELrel. 03, Created)
 DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Integrin beta G subunit.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinozoa;
 OC Echinoidea; Euechinozoa; Echinacea; Echinacea; Strongylocentrotidae;
 OX NCBI_TaxID=7668;
 [1] _____
 RN SEQUENCE FROM N.A.
 RP Marsden M., Burke R.D.;
 RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
 CC BONDS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
 DR EMBL; U77584; AAB39739.1; -;
 DR EMBL; U77587; AAB39741.1; -;


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DR HSPD, P05106, 13V2.
DR InterPro: IPR000561, EGF-like.
DR InterPro: IPR003361, Integrin B.
DR InterPro: IPR001869, Integrin beta_C.
DR InterPro: IPR003659, plexin-like.
DR InterPro: IPR002035, VWF_A.
DR Pfam: PF00362, Integrin_B.1.
DR Pfam: PD001811, Integrin_B.1.
DR SMART: SM00187, INB.1.
DR SMART: SM00423, PSI.1.
DR SMART: SM00327, VMA.1.
DR PROSITE: PS00022, EGF_1, UNKNOWN_2.
DR PROSITE: PS01186, EGF_2, UNKNOWN_1.
DR PROSITE: PS00243, INTEGRIN_BETA_2.
DR Cell adhesion: Cytoskeleton; Glycoprotein; Integrin; Repeat;
KW Transmembrane.
SQ SEQUENCE 783 AA; 85530 MW; B8045C6FED86FB2 CRC64;

Query Match 18.9%; Score 76.5; DB 5; Length 783;
Best Local Similarity 33.3%; Pred. No. 0.11; 24; Indels 5; Gaps 3;
Matches 19; Conservative 9; Mismatches 24;

OY 13 TCMSKCTICNHSQRTCAFCRCRKEQKFTY-DHLRDCISCSICGQHPK-QCAIF 66
DB 592 TCMTGDIICNGEVCICGE--CKNAGSYRGALCODCPTCSGQCSRMEEVCQKAF 646

RESULT 5
OY 074567 PRELIMINARY; PRT; 704 AA.
ID 074567
AC 074567, 1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Q174 protein.
GN Q174.
OS Trichoderma harzianum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; mitosporic Hyphomycetes; Trichoderma.
OX NCBI_TaxID=5544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 2413; PubMed=9600944;
RX MEDLINE=9826335; Pinot-Toro J.A., Jose A., Lobell A., Benitez T.;
RA Rey M., Ohno S.A., Pinot-Toro J.A., Jose A., Lobell A., Benitez T.;
RT "Unexpected homology between inducible cell wall protein of
RT filamentous fungi and BR3 salivary protein of the insect Chironomus.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6212-6216(1998).
DR EMBL: X95671; CAA64974.1;
DR InterPro: IPR000561; EGF-like.
DR PROSITE: PS01186; EGF_2; 1.
KW EGF-like domain; Glycoprotein.
SQ SEQUENCE 704 AA; 77925 MW; 63414BDDEC365EBC CRC64;

Query Match 18.6%; Score 75.5; DB 3; Length 704;
Best Local Similarity 28.6%; Pred. No. 0.13;
Matches 28; Conservative 9; Mismatches 20; Indels 41; Gaps 9;

OY 1 CPEQYWDPLGTGCMSCCK-TI-----CNH-----QSQRCAAFCCRKEQKFTYDH 44
DB 509 CPDQYWD---GSKCACPYGTVDGKKNCDCKGKXHPDSNOKCV---CNK-QSEVYDS 561
OY 45 LRDICSCASICGQH-----PKCAVFC 67
DB 562 KSKTC-SCPD--GGYWDGSKCACPYGKWDGKQCVNRC 596

RESULT 6
OY 09BPS2 PRELIMINARY; PRT; 1069 AA.
AC 09BPS2
ID 09BPS2
DT 01-JUN-2001 (Tremblrel. 17, Created)

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DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Laminin (Fragment).
DE Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Plekoptera; Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyoptera;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang W., Zemskov R.A., Imai N., Iwanaga M., Suzuki M.G.;
RT "Characterization of interaction between Bombyx mori
RT nucleopolyhedrovirus BRO-A and host LAMININ-like protein.";
RT Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RL EMBL: AB046363; F02468; 1178.
DR HSPD, P02468, 1178.
DR InterPro: IPR000561, EGF-like.
DR InterPro: IPR002049, Laminin_EGF.
DR Pfam: PF00051, Laminin_EGF.
DR PRINTS: PR00011, EGF_LAMININ.
DR SMART: SM00180, EGF_Lam; 8.
DR SMART: SM00001, EGF_Like; 1.
DR PROSITE: PS00022, EGF_1, UNKNOWN_6.
DR PROSITE: PS01186, EGF_2, 1.
DR PROSITE: PS01248, LAMININ_TYPE_EGF, UNKNOWN_8.
KW EGF-like domain; Glycoprotein.
FT NON TER 1
SQ SEQUENCE 1069 AA; 118894 MW; DF40F37A0CCA79A4 CRC64;

Query Match 18.5%; Score 75; DB 5; Length 1069;
Best Local Similarity 29.7%; Pred. No. 0.23; 28; Indels 12; Gaps 3;
Matches 19; Conservative 5; Mismatches 28;

OY 1 CPEQYWDPLGTGCMSCKTCNHSQRTCAFCRCRKEQKFTYDHLRDCISCSICGQH 59
DB 257 CADNYGDPPIRGCEKCE--CNENIDITKPGNC-----DYTGKCLQCLNTAGEH 305
OY 60 PKQC 63
DB 306 CDVC 309

RESULT 7
OY 09D2H5 PRELIMINARY; PRT; 723 AA.
ID 09D2H5
AC 09D2H5, 2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE 4930486B16R1K protein.
GN 4930486B16R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851; Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Komno H., Adachi J., Fukuda S.,
RA Aikawa T., Hara A., Fukunishi Y., Kiyosawa H., Kondo S., Yamana K.I.,
RA Aizawa K., Izawa M., Nishi K., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Katoda K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Perle G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Watanabe M.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Butt C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli S., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RESULT 11
Q24301 ID Q24301 PRELIMINARY; PRT; 932 AA.
AC Q24301 Q24301
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE PACE4A (Fragment).
GN PCSK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutaria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RA STRAIN=ICR; TISSUE=LIVER;
RA Nakayama K.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RA STRAIN=ICR; TISSUE=LIVER;
RA Hosaka M.; Murakami K.; Nakayama K.;
RL "PAC4A is a ubiquitous endoprotease that has similar but not
RT identical substrate specificity to other kex2-like processing
RT endoproteases."
RT Biomed. Res. 15:383-390(1994).
DR EMBL; D50060; BA087771.1; -.
DR HSSP; Q99405; IMPT.
DR MEROPS; S08.075; -.
DR MGDI; MGI:102897; PCBK6.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR000209; Peptidase-S8.
DR InterPro; IPR002884; P domain.
DR InterPro; IPR000842; ZnF_C2H2.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P domain; 1.
DR SMART; SM00181; EGF_2.
DR SMART; SM00261; FU; 5.
DR SMART; SM00001; EGF-like; 1.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR NON_TER.
SQ SEQUENCE 932 AA; 103310 MW; 15660179C8CAC72E CRC64;

Query Match 17.7%; Score 71.5; DB 11; Length 932;
Best Local Similarity 29.6%; Pred. No. 0.57; 24; Indels 7; Gaps 3;
Matches 16; Conservative 7; Mismatches 24;

QY 14 CMSGCT-ICNHQSORTCAFCCKEKGKFFDHLRDCISC--ASTICGQHPRQC 63
DB 727 CLSCRGFYHNETTCVTLCT---PGLVADBSQRLCLRHPCQKCVDFEPC 777

RESULT 12
Q8S2S2 ID Q8S2S2 PRELIMINARY; PRT; 1376 AA.
AC Q8S2S2 Q8S2S2
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE L3010182P.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M.; Brokstein P.; Hong L.; Aspayani A.; Carlson J.;
RA Champe M.; Chavez C.; Dorenek V.; Dresnek D.; Farfan D.; Fise E.;
RA George R.; Gonzalez M.; Guerin H.; Krommiller B.; Li P.; Liao G.;
RA Miranda A.; Mungai C.J.; Nunoo J.; Pacleb J.; Paragas V.; Park S.;
RA Patel S.; Phouanavong S.; Wan K.; Yu C.; Lewis S.E.; Rubin G.M.;
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY070553; AAL48024.1; -.
SQ SEQUENCE 1376 AA; 149716 MW; B6704BA89A3A08FB CRC64;

Query Match 17.7%; Score 71.5; DB 5; Length 1376;
Best Local Similarity 32.1%; Pred. No. 0.82; 23; Indels 9; Gaps 3;
Matches 18; Conservative 6; Mismatches 23;

QY 1 CPEEQYWDPLGTGMSGCTICNHQSORTC--APCRKEGCKFY-DHLRDCISC 52
DB 1083 CLASSQYDTSATCKTC---HDSGRSCFGPGGFCGCKGCVPLHLDQINSQVSC 1133

RESULT 13
Q24301 ID Q24301 PRELIMINARY; PRT; 1679 AA.
AC Q24301 Q24301
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE FUR2 protein.
GN FUR2 OR DFUR2 OR CG4235 OR CG18734.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEHLIN=20196006; PubMed=10731132;
RA Adams M.D.; Gelinkner S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Amaniatis P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.;
RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Anderson S.N.;
RA Sutton G.G.; Mortan J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers J.-H.C.; Blazey R.G.; Champe M.; Pfeiffer B.D.;
RA Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
RA April J.F.; Aspayani A.; An H.-J.; Andrews-Pfannkoch C.; Baldwin D.;
RA Ballow R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
RA Beeson K.Y.; Benos P.V.; Bertan B.P.; Bhandari P.; Bolshakov S.;
RA Borokova D.; Botchan M.R.; Bouck J.; Brokstein P.; Brotler P.;
RA Burtis K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
RA Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
RA de Pablo B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.;
RA Dodson K.; Evans J.; Fouts D.E.; Fouts R.; Dugan-Rocha S.; Dunn P.;
RA Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferreira S.; Fleischmann W.;
RA Fowler C.; Gabrielian A.E.; Gary N.S.; Gelbart W.M.; Glasser K.;
RA Glodde A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
RA Harris N.L.; Harvey D.; Heiman T.J.; Hernandez J.R.; Houck J.;
RA Hostin D.; Houston K.A.; Howard T.J.; Wei M.-H.; Ibegwam C.;
RA Jaiswal M.; Kalush F.; Kapen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.;
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai X.;
RA Laekko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.;
RA Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
RA Merkulov G.; Milshina N.V.; Mobarry C.; Morris J.; Moshirei A.;
RA Mount S.M.; Moy M.; Murphy B.; Murphy L.; Murty D.M.; Nelson D.L.;
RA Nelson D.L.; Nelson K.A.; Niken K.; Pollard J.; Pui V.; Reese M.G.;
RA Palazzolo M.; Piatman K.S.; Pan S.; Sanders R.D.; Scheeler F.; Shen T.;
RA Reinert K.; Remington K.; Sanders R.D.; Scheeler F.; Shen T.;
RA Shue B.C.; Siden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.;
RA Spier B.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.; Wang X.;
RA Svirskas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.;
RA Wang Z.-Y.; Wasserman D.A.; Weinstein G.M.; Weissbach J.;
RA Williams S.M.; Woodman T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.;

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Job time : 20.9749 secs

Search completed: January 7, 2003, 09:40:12
Job time : 20.9749 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 7, 2003, 09:35:14 ; Search time 8.22807 Seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405
Sequence: 1 CPEQYMDPLGTGTCMCKTI.....DCISCASICGHPKOCAYFC 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCIVS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	97.0	166	2	US-08-810-572A-6
2	393	97.0	166	4	US-09-290-333-6
3	393	97.0	293	2	US-08-810-572A-2
4	393	97.0	293	4	US-09-290-333-2
5	76.5	18.9	325	4	US-08-915-795-3
6	76.5	18.9	354	4	US-08-915-795-5
7	74.5	18.4	969	2	US-08-284-941-2
8	74.5	18.4	969	2	US-08-447-642-2
9	74.5	18.4	969	4	US-09-236-503-2
10	74.5	18.4	969	5	PCT-US93-02147A-2
11	70	17.3	704	4	US-09-590-656-1
12	70	17.3	977	4	US-08-323-674-2
13	70	17.3	1124	1	US-08-323-674-2
14	70	17.3	1124	5	PCT-US93-06093-2
15	69.5	17.2	75	2	US-08-465-380-6
16	69.5	17.2	75	2	US-08-465-380-41
17	69.5	17.2	75	2	US-08-480-478-35
18	69.5	17.2	75	2	US-08-486-397-41
19	69.5	17.2	75	2	US-08-486-397-6
20	69.5	17.2	75	2	US-08-486-399-41
21	69.5	17.2	75	2	US-08-486-399-6
22	69.5	17.2	75	2	US-08-461-965-6
23	69.5	17.2	75	2	US-08-461-965-41
24	69.5	17.2	75	2	US-08-326-110A-35
25	69.5	17.2	75	2	US-08-634-641-6
26	69.5	17.2	75	2	US-08-634-641-41
27	69.5	17.2	75	3	US-09-249-471-6

28	69.5	17.2	75	3	US-09-249-471-41	Sequence 41, Appl
29	69.5	17.2	75	3	US-09-249-472-6	Sequence 6, Appl
30	69.5	17.2	75	3	US-09-249-472-41	Sequence 41, Appl
31	69.5	17.2	75	3	US-09-249-451-6	Sequence 6, Appl
32	69.5	17.2	75	3	US-09-249-451-41	Sequence 41, Appl
33	69.5	17.2	75	3	US-08-809-455-6	Sequence 6, Appl
34	69.5	17.2	75	3	US-08-809-455-41	Sequence 41, Appl
35	69.5	17.2	75	3	US-09-249-461-6	Sequence 6, Appl
36	69.5	17.2	75	3	US-09-249-461-41	Sequence 41, Appl
37	69.5	17.2	75	3	US-09-249-448-41	Sequence 6, Appl
38	69.5	17.2	75	3	US-09-249-448-6	Sequence 41, Appl
39	69.5	17.2	79	2	US-08-465-380-8	Sequence 8, Appl
40	69.5	17.2	79	2	US-08-480-478-37	Sequence 37, Appl
41	69.5	17.2	79	2	US-08-486-397-8	Sequence 8, Appl
42	69.5	17.2	79	2	US-08-486-399-8	Sequence 8, Appl
43	69.5	17.2	79	2	US-08-461-965-8	Sequence 8, Appl
44	69.5	17.2	79	2	US-08-326-110A-37	Sequence 37, Appl
45	69.5	17.2	79	2	US-08-634-641-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 97.0%; Score 393; DB 2; Length 166;
Best Local Similarity 94.4%; Pred. No. 8.7e-35;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLLTGCMSCCTICNHQSORTCAAF- ---CRKEQKGYDHLRLDCISCASIC 56
 Db 34 CPEQYWDPLLTGCMSCCTICNHQSORTCAAF- ---CRKEQKGYDHLRLDCISCASIC 93
 Qy 57 GQHPKQCAAYFC 67
 Db 94 GQHPKQCAAYFC 104

RESULT 2

US-09-290-333-6
 ; Sequence 6, Application US/09290333
 ; Patent No. 6316222
 ; GENERAL INFORMATION:
 ; APPLICANT: Bram, Richard J.
 ; von Bulow, Gotz
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
 ; THEREOF

NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/290,333
 FILING DATE: 12-Apr-1999
 CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-290-333-6

Query Match 97.0%; Score 393; DB 4; Length 166;

Best Local Similarity 94.4%; Pred. No. 8.7e-35; Mismatches 0; Indels 4; Gaps 1;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Qy 1 CPEQYWDPLLTGCMSCCTICNHQSORTCAAF- ---CRKEQKGYDHLRLDCISCASIC 56
 Db 34 CPEQYWDPLLTGCMSCCTICNHQSORTCAAF- ---CRKEQKGYDHLRLDCISCASIC 93
 Qy 57 GQHPKQCAAYFC 67
 Db 94 GQHPKQCAAYFC 104

RESULT 3

US-08-810-572A-2
 ; Sequence 2, Application US/08810572A
 ; Patent No. 5969102
 ; GENERAL INFORMATION:
 ; APPLICANT: Bram, Richard J.
 ; von Bulow, Gotz
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
 ; THEREOF

NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/810,572A
 FILING DATE: 28-FEB-1997
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1340-1-007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 293 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-810-572A-2

Query Match 97.0%; Score 393; DB 2; Length 293;
 Best Local Similarity 94.4%; Pred. No. 1.5e-34;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLLTGCMSCCTICNHQSORTCAAF- ---CRKEQKGYDHLRLDCISCASIC 56
 Db 34 CPEQYWDPLLTGCMSCCTICNHQSORTCAAF- ---CRKEQKGYDHLRLDCISCASIC 93

Qy 57 GQHPKQCAAYFC 67
 Db 94 GQHPKQCAAYFC 104

RESULT 4

US-09-290-333-2
 ; Sequence 2, Application US/09290333
 ; Patent No. 6316222
 ; GENERAL INFORMATION:
 ; APPLICANT: Bram, Richard J.
 ; von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
 CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
 THEREOF
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290.333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 97.0%; Score 393; DB 4; Length 293;
Best local Similarity 94.4%; Pred. No. 1.5e-34;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLGTGMSCKTICNHOSQRTCAFC---CKRKGKPYDHLRLDRCISCASTG 56
DB 34 CPEQYWDPLGTGMSCKTICNHOSQRTCAFCRSKRECKFYDHLRLDRCISCASTG 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104

RESULT 5
US-08-915-795-3
Sequence 3, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STRAKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915.795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
US-08-915-795-3

Query Match 18.9%; Score 76.5; DB 4; Length 325;
Best local Similarity 24.8%; Pred. No. 0.577; 22; Indels 57; Gaps 7;
Matches 28; Conservative 6; Mismatches 22;

QY 1 CPEQYWDPLGTGMSCKTICNHOSQRTCAFC---CKRKGKPYDHLRLDRCISCASTG 56
DB 193 CPEQYWDPLGTGMSCKTICNHOSQRTCAFCRSKRECKFYDHLRLDRCISCASTG 251
QY 24 -GQHPKQCAVFC 67
DB 252 LQHPKQCAVFC 104

RESULT 6
US-08-915-795-5
Sequence 5, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STRAKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915.795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
US-08-915-795-5
Query Match 18.4%; Score 76.5; DB 4; Length 354;
Best Local Similarity 24.8%; Pred. No. 0.62; 22; Indels 57; Gaps 7;
Matches 28; Conservative 6; Mismatches 22; Indels 57; Gaps 7;

Qy 1 CPERQYWD-----PLIGT-----CMSCKTCINH- 23
Db 222 CPIDMLWSNKKCVLOEENPLAGTEDSHLQEPALCGPHMFEDRCECV-CKTPCPKD 280

Qy 24 --QSORTCAAF-----CCRKEQGFYDHL--RDCISCASICQHPKQCA 64
Db 281 LIQHPKNCSCFECKESLETCQK-----HKLFPDTCSCEDRCDFHTRPCA 326

RESULT 7
US-08-284-941-2
; Sequence 2, Application US/08284941
; Patent No. 5863756
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; APPLICANT: KIEFER, MICHAEL C
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
; TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,941
; FILING DATE: 2 August 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-284-941-2
Query Match 18.4%; Score 74.5; DB 2; Length 969;
Best Local Similarity 27.8%; Pred. No. 2.6;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

Qy 14 CMSCKT-ICNHQSORTCAAFCCRKEQGFYDHLRLDCISC---ASICGQHPKQC 63
Db 764 CLSCRRGFYHHQEMNTCVTLCL---PAGFYADESQKNCLKCHPSCKKCVDEPEKC 814

RESULT 9
US-09-236-503-2
; Sequence 2, Application US/09236503
; Patent No. 6277590
; GENERAL INFORMATION:
; APPLICANT: Barr, Philip J
; APPLICANT: Kiefer, Michael C
; TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
; TITLE OF INVENTION: Polypeptides in Cells
; FILE REFERENCE: CHIR-009/04US
; CURRENT APPLICATION NUMBER: US/09/236,503
; CURRENT FILING DATE: 1999-01-25
; EARLIER APPLICATION NUMBER: 08/447,642
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: 08/284,941
; EARLIER FILING DATE: 1994-08-02
; EARLIER APPLICATION NUMBER: 07/848,629

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/ EARLIER FILING DATE: 1992-03-09
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 969
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-236-503-2

Query Match
Best Local Similarity 18.4%; Score 74.5; DB 4; Length 969;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

OY 14 CMSGKT-ICNHGQRTCAFCCKEKGKFDHLRDCISC--ASICGQHPKQC 63
DB 764 CLSCRRGFYHGHQMTCTVLTCL--PAGFYADESQKNCKLKCHPSCKKCVDEPERK 814

RESULT 10
PCT-US93-02147A-2
/ Sequence 2, Application PC/TUS9302147A
/ GENERAL INFORMATION:
/ APPLICANT: BARR, PHILIP J
/ APPLICANT: KIEFER, MICHAEL C
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
/ TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
/ STREET: FIVE PALO ALTO SQUARE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/02147A
/ FILING DATE: 19930309
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/848,629
/ FILING DATE: 09-MAR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: NEELEY PH.D., RICHARD L
/ REGISTRATION NUMBER: 30092
/ REFERENCE/DOCKET NUMBER: CHIR-009/0005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 494-7622
/ TELEFAX: (415) 857-0663
/ TELEX: 380816 COOLEY PA
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 969 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
PCT-US93-02147A-2

Query Match
Best Local Similarity 18.4%; Score 74.5; DB 5; Length 969;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

OY 14 CMSGKT-ICNHGQRTCAFCCKEKGKFDHLRDCISC--ASICGQHPKQC 63
DB 764 CLSCRRGFYHGHQMTCTVLTCL--PAGFYADESQKNCKLKCHPSCKKCVDEPERK 814

RESULT 11
US-09-590-656-2
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/ Sequence 2, Application US/09590656
/ Patent No. 6413932
/ GENERAL INFORMATION:
/ APPLICANT: Cerretti, Douglas P.
/ APPLICANT: Borges, Luis G.
/ APPLICANT: Fanslow, III, William C.
/ TITLE OF INVENTION: 'TEK ANTAGONISTS
/ FILE REFERENCE: 2900-A
/ CURRENT APPLICATION NUMBER: US/09/590,656
/ PRIOR FILING DATE: 2000-06-07
/ PRIOR FILING DATE: 1999-06-07
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 704
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-590-656-2

Query Match
Best Local Similarity 17.3%; Score 70; DB 4; Length 704;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;

OY 3 BEQYWDP---LIGTCM-----SCKTICN-HQSRTCAFCCKR 36
DB 212 EAQKMGPECNHLCYACNNNGVCHEDTGEICOPGFMGRTCEKXCELHTFRTCKERSGQ 271
OY 37 EQGKFDHLRDCISCASICGQHPKQCAVFC 67
DB 272 EGCKSYVFCLEPDYGCSCATGWKGLQCNEAC 302

RESULT 12
US-09-590-656-1
/ Sequence 1, Application US/09590656
/ Patent No. 6413932
/ GENERAL INFORMATION:
/ APPLICANT: Cerretti, Douglas P.
/ APPLICANT: Borges, Luis G.
/ APPLICANT: Fanslow, III, William C.
/ TITLE OF INVENTION: 'TEK ANTAGONISTS
/ FILE REFERENCE: 2900-A
/ CURRENT APPLICATION NUMBER: US/09/590,656
/ PRIOR FILING DATE: 2000-06-07
/ PRIOR FILING DATE: 1999-06-07
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 977
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-590-656-1

Query Match
Best Local Similarity 17.3%; Score 70; DB 4; Length 977;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;

OY 3 BEQYWDP---LIGTCM-----SCKTICN-HQSRTCAFCCKR 36
DB 212 EAQKMGPECNHLCYACNNNGVCHEDTGEICOPGFMGRTCEKXCELHTFRTCKERSGQ 271
OY 37 EQGKFDHLRDCISCASICGQHPKQCAVFC 67
DB 272 EGCKSYVFCLEPDYGCSCATGWKGLQCNEAC 302

RESULT 13
US-08-323-474-2
/ Sequence 2, Application US/08323474
/ Patent No. 547860
/ GENERAL INFORMATION:
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APPLICANT: Ziegler, Steven P.
TITLE OF INVENTION: NOVEL TYROSINE KINASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/323,474
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,600
FILING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-474-2

Query Match 17.3%; Score 70; DB 1; Length 1124;
Best Local Similarity 26.4%; Pred. No. 9.1;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;
QY 3 EQQYDHP-----LLGTCM-----SKTTCN-HOSORTCAAFCCRK 36
DB 212 EAQKWGPCNHLCTACMNVGCHDTGECICPPGFMGRTCEKACELHTFGRTCKERCSCG 271
QY 37 EQQFYDHLRDCISCASICGQHPKQCAAYFC 67
DB 272 EGCKSYVFLPDPYGCSCATGWKGLQCNEAC 302

RESULT 14
PCT-US93-06093-2
Sequence 2, Application PC/TUS9306093
GENERAL INFORMATION:
APPLICANT: Ziegler, Steven P.
TITLE OF INVENTION: NOVEL TYROSINE KINASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06093
FILING DATE: 19930625

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,600
FILING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-06093-2

Query Match 17.3%; Score 70; DB 5; Length 1124;
Best Local Similarity 26.4%; Pred. No. 9.1;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;
QY 3 EQQYDHP-----LLGTCM-----SKTTCN-HOSORTCAAFCCRK 36
DB 212 EAQKWGPCNHLCTACMNVGCHDTGECICPPGFMGRTCEKACELHTFGRTCKERCSCG 271
QY 37 EQQFYDHLRDCISCASICGQHPKQCAAYFC 67
DB 272 EGCKSYVFLPDPYGCSCATGWKGLQCNEAC 302

RESULT 15
US-08-465-380-6
Sequence 6, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Anacyclostoma caninum
US-08-465-380-6

Query Match 17.2%; Score 69.5; DB 2; Length 75;
Best Local Similarity 27.9%; Pred. No. 0.79; 28; Indels 11; Gaps 4;
Matches 19; Conservative 10; Mismatches 28; Indels 11; Gaps 4;
QY 2 PE--EQYWDPLIGTCMSCKTICNHOSQ--TCAAFCCRK-----EQKFPDHLRDCIS 51
DB 4 PEGGENEMLDVCGTKKPCAKCSEEEEDDPICRSFSGPGPACVCEDEGFRDVTIVIGDCVK 63
QY 52 CASICGQH 59
DB 64 -EEECDOH 70

Search completed: January 7, 2003, 09:42:08
Job time : 9.22807 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:40:20 ; Search time 5.03759 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405

Sequence: 1 CPEEQYMDPLIGTMSCKTI.....DCISGASICGHPKQCAVFC 67

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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6/ptodata/1/pubpa/US06_NEM_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpa/US10_NEM_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	67	10 US-09-854-864-16	Sequence 16, Appl
2	393	97.0	156	10 US-09-854-864-15	Sequence 15, Appl
3	393	97.0	291	9 US-09-779-050A-43	Sequence 43, Appl
4	393	97.0	291	9 US-09-779-050A-42	Sequence 42, Appl
5	393	97.0	293	9 US-10-084-971-2	Sequence 2, Appl
6	393	97.0	293	10 US-09-879-919-22	Sequence 22, Appl
7	393	97.0	293	10 US-09-854-864-14	Sequence 14, Appl
8	393	97.0	293	10 US-09-861-376-2	Sequence 18, Appl
9	393	97.0	397	10 US-09-854-864-18	Sequence 20, Appl
10	313	77.3	59	10 US-09-854-864-20	Sequence 46, Appl
11	304	50.4	38	9 US-09-779-050A-46	Sequence 45, Appl
12	201	49.6	37	9 US-09-779-050A-45	Sequence 13, Appl
13	105	25.9	81	10 US-09-854-864-13	Sequence 54, Appl
14	84.5	20.9	220	10 US-10-042-141-54	Sequence 54, Appl
15	84.5	20.9	220	10 US-09-726-643-54	Sequence 3, Appl
16	76.5	18.9	207	9 US-10-077-137-3	Sequence 3, Appl
17	76.5	18.9	207	9 US-10-077-137-3	Sequence 2, Appl
18	76.5	18.9	354	10 US-09-956-095-2	Sequence 11, Appl
19	76.5	18.9	354	10 US-09-219-345A-11	Sequence 11, Appl

20	76.5	18.9	354	10 US-09-795-006A-119	Sequence 119, App
21	76.5	18.9	362	12 US-10-139-876-4	Sequence 4, Appl
22	76	18.8	77	10 US-09-840-795-17	Sequence 17, Appl
23	76	18.8	231	10 US-09-840-795-19	Sequence 19, Appl
24	76	18.8	299	9 US-10-119-466-12	Sequence 12, Appl
25	75	18.5	1497	10 US-09-060-854B-2	Sequence 2, Appl
26	72	17.8	100	10 US-09-864-761-47388	Sequence 47388, A
27	71	17.5	1617	10 US-09-784-358-16	Sequence 16, Appl
28	71	17.5	1691	10 US-09-784-358-2	Sequence 2, Appl
29	67.5	16.7	3084	10 US-09-938-275-4	Sequence 4, Appl
30	66.5	16.4	34	10 US-09-854-864-7	Sequence 6, Appl
31	66.5	16.4	51	10 US-09-854-864-6	Sequence 7, Appl
32	66.5	16.4	58	10 US-09-854-864-5	Sequence 5, Appl
33	66.5	16.4	181	10 US-09-854-864-1	Sequence 1, Appl
34	66.5	16.4	184	9 US-10-077-438-1	Sequence 7, Appl
35	66.5	16.4	184	9 US-10-077-438-7	Sequence 1, Appl
36	66.5	16.4	184	9 US-10-077-137-7	Sequence 7, Appl
37	66.5	16.4	283	10 US-09-854-864-9	Sequence 9, Appl
38	66.5	16.4	283	10 US-09-725-433-2	Sequence 13, Appl
39	65.5	16.2	358	9 US-09-852-203A-13	Sequence 2, Appl
40	65.5	16.2	358	12 US-10-139-876-4	Sequence 16, App
41	65.5	16.0	292	10 US-09-745-763-166	Sequence 2, Appl
42	65	16.0	4679	10 US-09-804-898-2	Sequence 1, Appl
43	64.5	15.9	798	9 US-10-117-295A-1	Sequence 1, Appl
44	64.5	15.8	162	10 US-09-798-789-13	Sequence 13, Appl
45	64	15.8	162	10 US-09-798-789-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA,
; TITLE OF INVENTION: BLS/AGP-3, AND TACI
; FILE REFERENCE: P-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match 100.0%; Score 405; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.8e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPEEQYMDPLIGTMSCKTICNHOSORTCAFCCKRKGKGFYHLADDCISGASICGHP 60
DB 1 CPEEQYMDPLIGTMSCKTICNHOSORTCAFCCKRKGKGFYHLADDCISGASICGHP 60
QY 61 KQCAVFC 67
DB 61 KQCAVFC 67
RESULT 2
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:


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; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-879-919-22

Query Match          97.0%; Score 393; DB 10; Length 293;
Best Local Similarity 94.4%; Pred. No. 1,5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLGTGCMCKTICNHOSQRTCAFC---CRKEQGFYDHLRDCISCASIC 56
DB 34 CPEQYWDPLGTGCMCKTICNHOSQRTCAFCRSLSCKREQGFYDHLRDCISCASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104

RESULT 7
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLIS/AGP-3, AND TACT
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-14

Query Match          97.0%; Score 393; DB 10; Length 293;
Best Local Similarity 94.4%; Pred. No. 1,5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLGTGCMCKTICNHOSQRTCAFC---CRKEQGFYDHLRDCISCASIC 56
DB 34 CPEQYWDPLGTGCMCKTICNHOSQRTCAFCRSLSCKREQGFYDHLRDCISCASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104
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RESULT 8
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PFS24P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-961-376-2

Query Match          97.0%; Score 393; DB 10; Length 293;
Best Local Similarity 94.4%; Pred. No. 1,5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLGTGCMCKTICNHOSQRTCAFC---CRKEQGFYDHLRDCISCASIC 56
DB 34 CPEQYWDPLGTGCMCKTICNHOSQRTCAFCRSLSCKREQGFYDHLRDCISCASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104

RESULT 9
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLIS/AGP-3, AND TACT
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-18

Query Match          97.0%; Score 393; DB 10; Length 397;
Best Local Similarity 94.4%; Pred. No. 1,9e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLGTGCMCKTICNHOSQRTCAFC---CRKEQGFYDHLRDCISCASIC 56
DB 34 CPEQYWDPLGTGCMCKTICNHOSQRTCAFCRSLSCKREQGFYDHLRDCISCASIC 93
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Qy 57 GQHPKQCAAYFC 67
Db 94 GQHPKQCAAYFC 104

RESULT 10
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match 77.3%; Score 313; DB 10; Length 59;
Best Local Similarity 93.2%; Pred. No. 2.2e-24;
Matches 55; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLLGTCMSCKTICNHQSORTCAAF----CRKEQKGYDHLRLDCISCASI 55
Db 1 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGYDHLRLDCISCASI 59

RESULT 11
US-09-779-050A-46
; Sequence 46, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 46
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-46

Query Match 50.4%; Score 204; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.7e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 CRKEQKGYDHLRLDCISCASICQHPKQCAAYFC 67
Db 2 CRKEQKGYDHLRLDCISCASICQHPKQCAAYFC 35

RESULT 12
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:

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; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 45
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-45

Query Match 49.6%; Score 201; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPEQYWDPLLGTCMSCKTICNHQSORTCAAF 33
Db 2 CPEQYWDPLLGTCMSCKTICNHQSORTCAAF 34

RESULT 13
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 25.9%; Score 105; DB 10; Length 81;
Best Local Similarity 30.0%; Pred. No. 0.00046;
Matches 21; Conservative 13; Mismatches 22; Indels 14; Gaps 4;

Qy 1 CPEQYWDPLLGTCMSCKTICNHQS-ORTCAAFCKRKEQKGYDHLRL--DCISCASICG 57
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCORYCC-----EYFDSLHACFCLRCS---- 51

Qy 58 QHPKQCAAYFC 67
Db 52 --PPTCQYCC 59

RESULT 14
US-10-042-141-54
; Sequence 54, Application US/10042141
; Publication No. US20020183503A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/10/042,141
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/7726,643

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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,725
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 54
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (170)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-042-141-54

Query Match
Best Local Similarity 20.9%; Score 84.5; DB 9; Length 220;
Matches 25; Conservative 10; Mismatches 27; Indels 35; Gaps 6;

QY 1 CPPE--QYMDPL-----LGTG-----MSCKTICNHQSORTCAFCCKRKE 37
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 CPETWVEIWMCMNSLGVFKKSDGWVGLGCCELAIALBCROACKOASSNDISKVCRKE 133
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 38 QGKPYDHLRDCT-----CASICGHPKOCAYFC 67
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 ----YENALFSCISRNMGSVCSSYAGHH-TNCREYC 165
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-09-726-643-54
; Sequence 54, Application US/09726643
; Patent No. US200202849A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/09/726,643
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,725
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 54
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (170)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-726-643-54

Query Match
Best Local Similarity 20.9%; Score 84.5; DB 10; Length 220;
Matches 25; Conservative 10; Mismatches 27; Indels 35; Gaps 6;

QY 1 CPPE--QYMDPL-----LGTG-----MSCKTICNHQSORTCAFCCKRKE 37
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 CPETWVEIWMCMNSLGVFKKSDGWVGLGCCELAIALBCROACKOASSNDISKVCRKE 133
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 38 QGKPYDHLRDCT-----CASICGHPKOCAYFC 67
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 ----YENALFSCISRNMGSVCSSYAGHH-TNCREYC 165
   ||| : : : : : : : : : : : : : : : : : : : : : : : : :

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Job time : 6.03759 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:38:19 ; Search time 8.73183 Seconds
(without alignments)
543.836 Million cell updates/sec

Title: US-09-855-158-16

Sequence: 1 CPEBYWDPPLGTCTCMSCCTI.....DCISCASICGHPKOCAYFC 67

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Gapop 10.0, Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending Patents_AA_New.*
1: /cgn2_6/prodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	97.0	166	6	US-10-293-816-6 Sequence 22, Appl
2	393	97.0	293	6	US-10-268-951-22 Sequence 2, Appl
3	393	97.0	293	6	US-10-258-368-1 Sequence 1, Appl
4	393	97.0	293	6	US-10-293-816-2 Sequence 2, Appl
5	393	97.0	301	6	US-10-358-368-12 Sequence 12, Appl
6	393	97.0	324	6	US-10-358-368-8 Sequence 8, Appl
7	393	97.0	366	6	US-10-358-368-6 Sequence 6, Appl
8	393	97.0	404	6	US-10-358-368-15 Sequence 15, Appl
9	393	97.0	34	1	PCT-US02-34376-14 Sequence 14, Appl
10	204	50.4	34	6	US-10-281-053-14 Sequence 14, Appl
11	204	49.6	33	1	PCT-US02-34376-13 Sequence 13, Appl
12	201	49.6	33	6	US-10-281-053-13 Sequence 13, Appl
13	201	18.9	325	6	US-10-274-953-3 Sequence 3, Appl
14	18.5	18.9	354	6	US-10-274-953-5 Sequence 5, Appl
15	75	18.5	1548	6	US-10-180-903-2 Sequence 2, Appl
16	74.5	18.4	685	5	US-09-724-676A-81464 Sequence 81464, A
17	74.5	18.4	685	5	US-09-724-676A-81464 Sequence 81464, A
18	74.5	18.4	687	5	US-09-724-676A-81462 Sequence 81462, A
19	74.5	18.4	687	5	US-09-724-676A-81462 Sequence 81462, A
20	74.5	18.4	700	5	US-09-724-676A-81463 Sequence 81463, A
21	74.5	18.4	700	5	US-09-724-676A-81463 Sequence 81463, A
22	74.5	18.4	700	5	US-09-724-676A-81463 Sequence 81463, A
23	74.5	18.4	700	5	US-09-724-676A-81463 Sequence 81463, A
24	74.5	18.4	713	5	US-09-724-676A-81467 Sequence 81467, A
25	74.5	18.4	713	5	US-09-724-676A-81467 Sequence 81467, A
26	74.5	18.4	733	5	US-09-724-676A-81444 Sequence 81444, A

27	74.5	18.4	733	5	US-09-724-676A-81444 Sequence 81444, A
28	74.5	18.4	735	5	US-09-724-676A-81442 Sequence 81442, A
29	74.5	18.4	735	5	US-09-724-676A-81442 Sequence 81442, A
30	74.5	18.4	748	5	US-09-724-676A-81443 Sequence 81443, A
31	74.5	18.4	748	5	US-09-724-676A-81443 Sequence 81443, A
32	74.5	18.4	748	5	US-09-724-676A-81443 Sequence 81443, A
33	74.5	18.4	748	5	US-09-724-676A-81443 Sequence 81443, A
34	74.5	18.4	752	5	US-09-724-676A-81457 Sequence 81457, A
35	74.5	18.4	752	5	US-09-724-676A-81455 Sequence 81455, A
36	74.5	18.4	754	5	US-09-724-676A-81458 Sequence 81458, A
37	74.5	18.4	760	5	US-09-724-676A-81458 Sequence 81458, A
38	74.5	18.4	761	5	US-09-724-676A-81447 Sequence 81447, A
39	74.5	18.4	761	5	US-09-724-676A-81447 Sequence 81447, A
40	74.5	18.4	778	5	US-09-724-676A-81453 Sequence 81453, A
41	74.5	18.4	778	5	US-09-724-676A-81453 Sequence 81453, A
42	74.5	18.4	780	5	US-09-724-676A-81451 Sequence 81451, A
43	74.5	18.4	780	5	US-09-724-676A-81451 Sequence 81451, A
44	74.5	18.4	780	5	US-09-724-676A-81451 Sequence 81451, A
45	74.5	18.4	780	5	US-09-724-676A-81451 Sequence 81451, A

ALIGNMENTS

```
RESULT 1
US-10-293-816-6
Sequence 6 Application US/10293816
GENERAL INFORMATION:
APPLICANT: Ikon, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
FILE REFERENCE: 44158/254623
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US/10/293,816
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-816-6
Query Match 97.0%; Score 393; DB 6; Length 166;
Best Local Similarity 94.4%; Pred. No. 1.8e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEBYWDPPLGTCTCMSCCTI-----CRKQGFYDHLDPDCTSCASIC 56
DB 34 CPEBYWDPPLGTCTCMSCCTI-----CRKQGFYDHLDPDCTSCASIC 93
QY 57 GQHPKOCAYFC 67
DB 94 GQHPKOCAYFC 104
RESULT 2
US-10-268-951-22
Sequence 22 Application US/10268951
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: P253P2
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/10/268,951
PRIOR FILING DATE: 2002-02-26
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; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22

Query Match          97.0%; Score 393; DB 6; Length 293;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFC-----CRKEQKGFYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFCRSLSCRKEQKGFYDHLRLDCISCASIC 93

QY 57 GOHPKQCAAYFC 67
Db 94 GOHPKQCAAYFC 104

RESULT 3
US-10-258-368-1
; Sequence 1, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-1

Query Match          97.0%; Score 393; DB 6; Length 293;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFC-----CRKEQKGFYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFCRSLSCRKEQKGFYDHLRLDCISCASIC 93

QY 57 GOHPKQCAAYFC 67
Db 94 GOHPKQCAAYFC 104
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RESULT 4
US-10-293-816-2
; Sequence 2, Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

Query Match          97.0%; Score 393; DB 6; Length 293;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFC-----CRKEQKGFYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFCRSLSCRKEQKGFYDHLRLDCISCASIC 93

QY 57 GOHPKQCAAYFC 67
Db 94 GOHPKQCAAYFC 104

RESULT 5
US-10-258-368-12
; Sequence 12, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-12

Query Match          97.0%; Score 393; DB 6; Length 301;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFC-----CRKEQKGFYDHLRLDCISCASIC 56
Db 42 CPEEQYWDPLLGTCMCKTICNHQSORTCAAFCAFCRSLSCRKEQKGFYDHLRLDCISCASIC 101

QY 57 GOHPKQCAAYFC 67
Db 102 GOHPKQCAAYFC 112
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RESULT 6
US-10-258-368-8
; Sequence 8 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Renner, Paul
; TITLE OF INVENTION: Tact As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-8

Query Match
Best Local Similarity 97.0%; Score 393; DB 6; Length 334;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYMDPLGTGMSCKTTCNHOSORTCAFC-----CRKQKGFYDHLRDCISCSIC 56
Db 25 CPEQYMDPLGTGMSCKTTCNHOSORTCAFCRSLSCKRQKGFYDHLRDCISCSIC 84
Qy 57 GQHPKQCAVFC 67
Db 85 GQHPKQCAVFC 95

RESULT 7
US-10-258-368-6
; Sequence 6 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Renner, Paul
; TITLE OF INVENTION: Tact As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-6

Query Match
Best Local Similarity 97.0%; Score 393; DB 6; Length 366;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYMDPLGTGMSCKTTCNHOSORTCAFC-----CRKQKGFYDHLRDCISCSIC 56
Db 57 CPEQYMDPLGTGMSCKTTCNHOSORTCAFCRSLSCKRQKGFYDHLRDCISCSIC 116
Qy 57 GQHPKQCAVFC 67
Db 117 GQHPKQCAVFC 127

RESULT 8
US-10-258-368-15
; Sequence 15 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Renner, Paul
; TITLE OF INVENTION: Tact As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-15

Query Match
Best Local Similarity 97.0%; Score 393; DB 6; Length 404;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYMDPLGTGMSCKTTCNHOSORTCAFC-----CRKQKGFYDHLRDCISCSIC 56
Db 51 CPEQYMDPLGTGMSCKTTCNHOSORTCAFCRSLSCKRQKGFYDHLRDCISCSIC 110
Qy 57 GQHPKQCAVFC 67
Db 111 GQHPKQCAVFC 121

RESULT 9
PCT-US02-34376-14
; Sequence 14 Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yangfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14/354,966
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-14

Query Match
Best Local Similarity 50.4%; Score 204; DB 1; Length 34;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 CRKQKGFYDHLRDCISCSICGQHPKQCAVFC 67
Db 1 CRKQKGFYDHLRDCISCSICGQHPKQCAVFC 34

RESULT 10
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US-10-281-053-14
; Sequence 14, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86
; CURRENT APPLICATION NUMBER: US/10/281,053
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-281-053-14
Query Match 50.4%; Score 204; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CRKEQGRFYDHLRLDCISCAISCGQHPKQCAAYFC 67
|||||
Db 1 CRKEQGRFYDHLRLDCISCAISCGQHPKQCAAYFC 34

RESULT 11
PCT-US02-34376-13
; Sequence 13, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens

PCT-US02-34376-13
Query Match 49.6%; Score 201; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPEEQYWDPLLGTCMSCKTICNHQSORTCAAF 33
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Db 1 CPEEQYWDPLLGTCMSCKTICNHQSORTCAAF 33

RESULT 12
US-10-281-053-13
; Sequence 13, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86
; CURRENT APPLICATION NUMBER: US/10/281,053
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-281-053-13
Query Match 49.6%; Score 201; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPEEQYWDPLLGTCMSCKTICNHQSORTCAAF 33
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Db 1 CPEEQYWDPLLGTCMSCKTICNHQSORTCAAF 33

RESULT 13
US-10-274-953-3
; Sequence 3, Application US/10274953
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/274,953
; FILING DATE: 22-Oct-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.

```

;
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-10-274-953-3

Query Match      18.9%; Score 76.5; DB 6; Length 325;
Best Local Similarity 24.8%; Pred. No. 0.23;
Matches 28; Conservative 6; Mismatches 22; Indels 57; Gaps 7;

QY 1 CPEQYWD-----PLIGT-----CMSCRTICNH- 23
DB 193 CPIMLWDSNCKCVLQENPLAGTETHSHLOEPALCGPHMFPEDRCBCV-CKTPCPKD 251
QY 24 --QSORTCAAF-----CCRKQGFYDHL--RDCISCAICGHPKQCA 64
DB 252 LIQHPKNCSCFECKESLETCCQK-----HKLPHPTCSCEDRCPPHTRPCA 297

RESULT 14
; US-10-274-953-5
; Sequence 5, Application US/10274953
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeeown, Edwards & Lemahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/274,953
; FILING DATE: 22-Oct-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-10-274-953-5

Query Match      18.9%; Score 76.5; DB 6; Length 354;
Best Local Similarity 24.8%; Pred. No. 0.25;
Matches 28; Conservative 6; Mismatches 22; Indels 57; Gaps 7;

QY 1 CPEQYWD-----PLIGT-----CMSCRTICNH- 23
DB 222 CPIDLWDSNCKCVLQENPLAGTETHSHLOEPALCGPHMFPEDRCBCV-CKTPCPKD 280
QY 24 --QSORTCAAF-----CCRKQGFYDHL--RDCISCAICGHPKQCA 64
DB 281 LIQHPKNCSCFECKESLETCCQK-----HKLPHPTCSCEDRCPPHTRPCA 326

RESULT 15
; US-10-180-903-2
; Sequence 2, Application US/10180903
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-10-180-903-2

Query Match      18.5%; Score 75; DB 6; Length 1548;
Best Local Similarity 25.0%; Pred. No. 1.1;
Matches 21; Conservative 5; Mismatches 34; Indels 24; Gaps 3;

QY 1 CPEQYWDPLIGTMSCKTICNHOS-----QRTCAAFCCRKQGFYD 43
DB 1152 CAAVEYWDGSHRCQPCRRKCSRGSPSEDQCYCPRETFLLNTTQVKEC---PEGYHTD 1208
QY 44 HLDRDCISCAIC-----GQHPKQC 63
DB 1209 KDSQOCVLCSSCRTEGPHSMQC 1232

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Job time : 9.73183 secs

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OM protein - protein seq, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 112.338 Seconds

(without alignments)
384,527 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405

Sequence: 1 CPEEGYMDPLGTGCMSCCKTI.....DCISCSICGHPKCAVFC 67

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Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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25: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	67	22	US-09-854-864-16
2	405	100.0	67	22	US-09-855-158-16
3	393	97.0	166	12	US-08-810-472-6
4	393	97.0	166	21	US-09-782-857-6
5	393	97.0	166	21	US-09-784-857A-6
6	393	97.0	166	22	US-09-854-864-15

7	393	97.0	166	22	US-09-855-158-15	Sequence 15, Appl
8	393	97.0	245	19	US-09-479-855-9	Sequence 9, Appl
9	393	97.0	245	18	US-09-562-225-9	Sequence 9, Appl
10	393	97.0	245	20	US-09-627-205-9	Sequence 9, Appl
11	393	97.0	245	21	US-09-724-341-9	Sequence 9, Appl
12	393	97.0	245	21	US-09-779-050A-43	Sequence 2, Appl
13	393	97.0	245	1	PCT-US00-07966-2	Sequence 2, Appl
14	393	97.0	245	1	PCT-US01-19028-22	Sequence 2, Appl
15	393	97.0	245	1	PCT-US02-16105-46	Sequence 2, Appl
16	393	97.0	245	12	US-08-810-572-2	Sequence 46, Appl
17	393	97.0	245	17	US-09-302-863-2	Sequence 2, Appl
18	393	97.0	245	17	US-09-479-856-6	Sequence 2, Appl
19	393	97.0	245	18	US-09-533-822-2	Sequence 2, Appl
20	393	97.0	245	19	US-09-569-245-6	Sequence 6, Appl
21	393	97.0	245	19	US-09-627-205-6	Sequence 6, Appl
22	393	97.0	245	21	US-09-724-341-2	Sequence 2, Appl
23	393	97.0	245	21	US-09-779-050A-42	Sequence 42, Appl
24	393	97.0	245	21	US-09-782-857-2	Sequence 2, Appl
25	393	97.0	245	21	US-09-782-857A-2	Sequence 2, Appl
26	393	97.0	245	22	US-09-848-295-4	Sequence 4, Appl
27	393	97.0	245	22	US-09-854-864-14	Sequence 14, Appl
28	393	97.0	245	22	US-09-855-158-14	Sequence 14, Appl
29	393	97.0	245	22	US-09-855-564-2	Sequence 2, Appl
30	393	97.0	245	22	US-09-879-912-22	Sequence 2, Appl
31	393	97.0	245	23	US-09-961-316-2	Sequence 2, Appl
32	393	97.0	245	23	US-10-008-065-8	Sequence 8, Appl
33	393	97.0	245	24	US-10-068-725-4	Sequence 8, Appl
34	393	97.0	245	24	US-10-084-971-2	Sequence 2, Appl
35	393	97.0	245	25	US-10-151-882-46	Sequence 46, Appl
36	393	97.0	245	25	US-10-152-363A-2	Sequence 2, Appl
37	393	97.0	245	25	US-10-152-363A-52	Sequence 52, Appl
38	393	97.0	245	25	US-10-152-363A-54	Sequence 54, Appl
39	393	97.0	245	25	US-10-152-363A-56	Sequence 56, Appl
40	393	97.0	245	25	US-10-152-363A-50	Sequence 50, Appl
41	393	97.0	245	25	US-09-854-864-18	Sequence 18, Appl
42	393	97.0	245	22	US-09-855-158-18	Sequence 20, Appl
43	393	97.0	245	22	US-09-854-864-20	Sequence 20, Appl
44	393	97.0	245	22	US-09-855-158-20	Sequence 20, Appl
45	393	97.0	245	22	US-09-855-158-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-854-864-16

Sequence 16, Application US/09854864

GENERAL INFORMATION:

APPLICANT: THELL, LARS EYDE

INVENTOR: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

PRIOR FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 16

LENGTH: 67

TYPE: PRT

ORGANISM: Homo sapiens

US-09-854-864-16

Query Match

Best Local Similarity 100.0%; Score 405; DB 22; Length 67;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPEEGYMDPLGTGCMSCCKTI...CNHOSORTCAFCCKKQKGFYDHLFDICISCSICGHP 60

Db 1 CPEQYWDPLLTGTCMCKTICNHOSQRTCAAFCKRQKGFYDHLRLDCISCSICGQHP 60
Qy 61 KQAYFC 67
Db 61 KQAYFC 67

RESULT 2
US-09-855-158-16
; Sequence 16, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27 US 60/214,591
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-16

Query Match 100.0%; Score 405; DB 22; Length 67;
Best Local Similarity 100.0%; Pred. No. 7e-35; Mismatches 0; Indels 0; Gaps 0;
Matches 67; Conservative 0

Qy 1 CPEQYWDPLLTGTCMCKTICNHOSQRTCAAFCKRQKGFYDHLRLDCISCSICGQHP 60
Db 1 CPEQYWDPLLTGTCMCKTICNHOSQRTCAAFCKRQKGFYDHLRLDCISCSICGQHP 60
Qy 61 KQAYFC 67
Db 61 KQAYFC 67

RESULT 3
US-08-810-572-6
; Sequence 6, Application US/08810572
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 28-FEB-1997
; APPLICATION NUMBER: US/08/810,572
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572-6

Query Match 97.0%; Score 393; DB 12; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33; Mismatches 0; Indels 4; Gaps 1;
Matches 67; Conservative 0

Qy 1 CPEQYWDPLLTGTCMCKTICNHOSQRTCAAFCKRQKGFYDHLRLDCISCSIC 56
Db 34 CPEQYWDPLLTGTCMCKTICNHOSQRTCAAFCKRQKGFYDHLRLDCISCSIC 93
Qy 57 GQHPKQAYFC 67
Db 94 GQHPKQAYFC 104

RESULT 4
US-09-782-857-6
; Sequence 6, Application US/09782857
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: US/09/782,857
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857-6

Query Match      97.0%; Score 393; DB 21; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY      1 CPEEQYMDPLGTGCMCKTICNHOSORTCAFC---CRKEQGFYDHLRDCISCSASIC 56
DB      34 CPEEQYMDPLGTGCMCKTICNHOSORTCAFCRSLSCKREQGFYDHLRDCISCSASIC 93
OY      57 GQHPKOCAYFC 67
DB      94 GQHPKOCAYFC 104

RESULT 5
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; THEREOF
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match      97.0%; Score 393; DB 21; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY      1 CPEEQYMDPLGTGCMCKTICNHOSORTCAFC---CRKEQGFYDHLRDCISCSASIC 56
DB      34 CPEEQYMDPLGTGCMCKTICNHOSORTCAFCRSLSCKREQGFYDHLRDCISCSASIC 93
OY      57 GQHPKOCAYFC 67
DB      94 GQHPKOCAYFC 104

RESULT 6
US-09-854-864-15
; Sequence 15, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; SOFTWARE: Patentin version 3.1
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match      97.0%; Score 393; DB 22; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY      1 CPEEQYMDPLGTGCMCKTICNHOSORTCAFC---CRKEQGFYDHLRDCISCSASIC 56
DB      34 CPEEQYMDPLGTGCMCKTICNHOSORTCAFCRSLSCKREQGFYDHLRDCISCSASIC 93
OY      57 GQHPKOCAYFC 67
DB      94 GQHPKOCAYFC 104

RESULT 7
US-09-855-158-15
; Sequence 15, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; YS/AGP-3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; SOFTWARE: Patentin version 3.1
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      97.0%; Score 393; DB 22; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
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Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 93
QY 57 GQHPKQCAAYFC 67
Db 94 GQHPKQCAAYFC 104

RESULT 8
US-09-479-856-9
; Sequence 9, Application US/09479856
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/09/479,856
; PRIOR FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,068
; EARLIER FILING DATE: 1999-01-07
; EARLIER FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-479-856-9

Query Match 97.0%; Score 393; DB 18; Length 245;
Best Local Similarity 94.4%; Pred. No. 4.3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100

RESULT 9
US-09-569-245-9
; Sequence 9, Application US/09569245
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/09/569,245
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-245-9
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Query Match 97.0%; Score 393; DB 19; Length 245;
Best Local Similarity 94.4%; Pred. No. 4.3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100

RESULT 10
US-09-627-206-9
; Sequence 9, Application US/09627206
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75C2
; CURRENT APPLICATION NUMBER: US/09/627,206
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/569,245
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-627-206-9

Query Match 97.0%; Score 393; DB 20; Length 245;
Best Local Similarity 94.4%; Pred. No. 4.3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLLTGTCMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100

RESULT 11
US-09-724-341-9
; Sequence 9, Application US/09724341
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IQBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/09/724,341
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
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; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 9
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-341-9

Query Match
Best Local Similarity 97.0%; Score 393; DB 21; Length 265;
Best Local Similarity 94.4%; Pred. No. 4.7e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLGTGCTMCKTICNHOSORTCAFC---CRKEGKFPYDHLRDCISCASIC 56
    |||
Db 34 CPEQYWDPLGTGCTMCKTICNHOSORTCAFCRSLSCKRKGKFPYDHLRDCISCASIC 93
    |||

Qy 57 GQHPKOCAYFC 67
    |||
Db 94 GQHPKOCAYFC 104
    |||

RESULT 12
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match
Best Local Similarity 97.0%; Score 393; DB 21; Length 291;
Best Local Similarity 94.4%; Pred. No. 5.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLGTGCTMCKTICNHOSORTCAFC---CRKEGKFPYDHLRDCISCASIC 56
    |||
Db 34 CPEQYWDPLGTGCTMCKTICNHOSORTCAFCRSLSCKRKGKFPYDHLRDCISCASIC 93
    |||

Qy 57 GQHPKOCAYFC 67
    |||
Db 94 GQHPKOCAYFC 104
    |||

RESULT 13
PCT-US00-07966-2
; Sequence 2, Application PC/TUS0007966
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF54PCT
; CURRENT APPLICATION NUMBER: PCT/US00/07966
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,599
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/188,208
; EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT

; ORGANISM: Homo sapiens
PCT-US00-07966-2

Query Match
Best Local Similarity 97.0%; Score 393; DB 1; Length 293;
Best Local Similarity 94.4%; Pred. No. 5.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLGTGCTMCKTICNHOSORTCAFC---CRKEGKFPYDHLRDCISCASIC 56
    |||
Db 34 CPEQYWDPLGTGCTMCKTICNHOSORTCAFCRSLSCKRKGKFPYDHLRDCISCASIC 93
    |||

Qy 57 GQHPKOCAYFC 67
    |||
Db 94 GQHPKOCAYFC 104
    |||

RESULT 14
PCT-US01-19026-22
; Sequence 22, Application PC/TUS0119026
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PR253PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19026
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19026-22

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Best Local Similarity 94.4%; Pred. No. 5.1e-33;
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Qy 57 GQHPKOCAYFC 67
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Db 94 GQHPKOCAYFC 104
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PCT-US02-16106-46
; Sequence 46, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF54PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16106-46

Query Match 97.0%; Score 393; DB 1; Length 293;
Best Local Similarity 94.4%; Pred. No. 5.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEEQYWDPLLGTCMSCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
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Db 34 CPEEQYWDPLLGTCMSCKTICNHQSORTCAAFCRSLSCRKEQKGYDHLRLDCISCASIC 93
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Qy 57 GOHPKQCAAYFC 67
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Db 94 GOHPKQCAAYFC 104
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Search completed: January 7, 2003, 09:53:21
Job time : 113.338 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 135.812 Seconds

(without alignments)
384.527 Million cell updates/sec

Title: US-09-855-158-13

Sequence: 1 CSQNEYPDSLHACIPCOLR.....SEYFDSLHACPATCPYC 81

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Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	498	100.0	81	US-09-855-158-13	Sequence 13, Appl
3	230.5	46.3	207	US-10-077-137-3	Sequence 3, Appl
4	230.5	46.3	207	US-10-077-438-3	Sequence 3, Appl
5	205	41.2	302	US-10-115-192-12	Sequence 12, Appl
6	205	41.2	302	US-60-215-688-12	Sequence 12, Appl

7	201.5	40.5	283	22	US-09-854-864-9	Sequence 9, Appl
8	201.5	40.5	283	22	US-09-855-158-9	Sequence 9, Appl
9	201	40.4	34	22	US-09-854-864-7	Sequence 7, Appl
10	201	40.4	34	22	US-09-855-158-7	Sequence 7, Appl
11	201	40.4	51	22	US-09-854-864-6	Sequence 6, Appl
12	201	40.4	51	22	US-09-855-158-6	Sequence 6, Appl
13	201	40.4	58	22	US-09-854-864-21	Sequence 21, Appl
14	201	40.4	58	22	US-09-855-158-21	Sequence 21, Appl
15	201	40.4	181	22	US-09-854-864-5	Sequence 5, Appl
16	201	40.4	181	22	US-09-855-158-5	Sequence 5, Appl
17	201	40.4	184	1	PCT-US00-04665-1	Sequence 1, Appl
18	201	40.4	184	1	PCT-US00-04925-1	Sequence 1, Appl
19	201	40.4	184	1	PCT-US02-16106-47	Sequence 47, Appl
20	201	40.4	184	18	US-09-479-856-8	Sequence 8, Appl
21	201	40.4	184	19	US-09-565-423-11	Sequence 11, Appl
22	201	40.4	184	19	US-09-565-245-8	Sequence 8, Appl
23	201	40.4	184	20	US-09-627-206-8	Sequence 8, Appl
24	201	40.4	184	21	US-09-724-341-4	Sequence 4, Appl
25	201	40.4	184	23	US-09-914-119A-1	Sequence 1, Appl
26	201	40.4	184	24	US-10-008-063-7	Sequence 7, Appl
27	201	40.4	184	24	US-10-068-725-2	Sequence 2, Appl
28	201	40.4	184	24	US-10-077-137-1	Sequence 1, Appl
29	201	40.4	184	24	US-10-077-137-7	Sequence 7, Appl
30	201	40.4	184	24	US-10-077-438-1	Sequence 1, Appl
31	201	40.4	184	24	US-10-077-438-7	Sequence 7, Appl
32	201	40.4	184	25	US-10-115-182-8	Sequence 8, Appl
33	201	40.4	184	25	US-10-115-883-47	Sequence 47, Appl
34	201	40.4	184	25	US-10-152-363A-27	Sequence 27, Appl
35	201	40.4	184	27	US-60-215-688-8	Sequence 8, Appl
36	201	40.4	192	21	US-09-758-471-5100	Sequence 5100, Ap
37	201	40.4	192	26	US-10-235-953-5100	Sequence 5100, Ap
38	201	40.4	288	1	PCT-US02-06518-120	Sequence 120, Appl
39	201	40.4	117	22	US-09-854-864-12	Sequence 12, Appl
40	153	30.7	117	22	US-09-855-164-12	Sequence 12, Appl
41	139.5	28.0	281	22	US-09-854-864-10	Sequence 10, Appl
42	139.5	28.0	281	22	US-09-855-164-10	Sequence 10, Appl
43	136	27.3	185	1	PCT-US00-04665-2	Sequence 2, Appl
44	136	27.3	185	1	PCT-US00-04925-2	Sequence 2, Appl
45	136	27.3	185	19	US-09-565-423-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-13
Sequence 13, Application US/09854864
GENERAL INFORMATION:
APPLICANT: THEIL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854, 864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204, 039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214, 591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 498; DB 22; Length 81;
Best Local Similarity 100.0%; Pred No. 3.2e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CSQNEYPDSLHACIPCOLRCSNTPPLTCRCYCEYFDSLHACIPCTCYCCP 60
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Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCRLCSPPTCQYCCF 60
QY 61 HSEYFDSLHACPPATCPYC 81
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Db 61 HSEYFDSLHACPPATCPYC 81
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RESULT 2
US-09-855-158-13
; Sequence 13, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

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Best Local Similarity 100.0%; Pred. No. 3.2e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCRLCSPPTCQYCCF 60

QY 61 HSEYFDSLHACPPATCPYC 81
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RESULT 3
US-10-077-137-3
; Sequence 3, Application US/10077137
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCWA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3
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Best Local Similarity 57.8%; Pred. No. 2.5e-12;
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QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHAC-PC-LRCSPPPTCQYC 58
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QY 59 CFHSEYFDSLHACPPATCPYC 81
Db 91 -----PPLTCQRYC 99
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RESULT 4
US-10-077-438-3
; Sequence 3, Application US/10077438
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCWA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3
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Query Match 46.3%; Score 230.5; DB 24; Length 207;
Best Local Similarity 57.8%; Pred. No. 2.5e-12;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHAC-PC-LRCSPPPTCQYC 58
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Db 46 CSQNEYFDSLHACIPQCLRCSSNTPPLTC-----LHACIPQCLRCSSNT----- 90

QY 59 CFHSEYFDSLHACPPATCPYC 81
Db 91 -----PPLTCQRYC 99
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RESULT 5
US-10-115-192-12
; Sequence 12, Application US/10115192
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCWA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
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/ PRIOR FILING DATE: 1999-10-06
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-115-192-12

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Best Local Similarity 67.8%; Pred. No. 6.1e-10;
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Db 31 CSONEYFDSLHACIPCOLRCSSNTPLTCORCYCNASVTNSVKGVDKHTHCP--PCPAP 87

RESULT 6
US-60-215-688-12
/ Sequence 12, Application US/60215688
/ GENERAL INFORMATION:
/ APPLICANT: BIOGEN, INC.
/ TITLE OF INVENTION: APRIL RECEPTOR AND USES THEREOF
/ FILE REFERENCE: A083 P3
/ CURRENT APPLICATION NUMBER: US/60/215,688
/ PRIOR FILING DATE: 2000-06-30
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-60-215-688-12

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Best Local Similarity 67.8%; Pred. No. 6.1e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;

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RESULT 7
US-09-854-864-9
/ Sequence 9, Application US/09854864
/ GENERAL INFORMATION:
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ PRIOR FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 283
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-9

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Best Local Similarity 60.6%; Pred. No. 1.2e-09;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;

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RESULT 8
US-09-855-158-9
/ Sequence 9, Application US/09855158
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
/ FILE REFERENCE: A-686A
/ CURRENT APPLICATION NUMBER: US/09/855,158
/ PRIOR FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 283
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-855-158-9

Query Match          40.5%; Score 201.5; DB 22; Length 283;
Best Local Similarity 60.6%; Pred. No. 1.2e-09;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;

Cy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORCYC-CEYFDSL-----LHACPC 47
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Cy 48 LRCSP 53
Db 64 -PCPAP 68

RESULT 9
US-09-854-864-7
/ Sequence 7, Application US/09854864
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ PRIOR FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-7

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Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORCYC 34
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SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

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Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-854-864-5
; Sequence 5, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, IARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 40.4%; Score 201; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 9e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 38

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Job time : 136.812 secs

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GenCore version 5.1.3
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Run on: January 7, 2003, 09:37:34 ; Search time 57.0075 Seconds

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Title: US-09-855-158-7

Sequence: 1 CSONEYFSLHACIPCOLRCSNTPPLTCORYC 34

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Maximum Match 100%

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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	34	22	US-09-854-864-7
2	201	100.0	34	22	US-09-855-158-7
3	201	100.0	51	22	US-09-854-864-6
4	201	100.0	51	22	US-09-854-158-6
5	201	100.0	58	22	US-09-854-864-21
6	201	100.0	58	22	US-09-855-158-21

7	201	100.0	81	22	US-09-854-864-13	Sequence 13, Appl
8	201	100.0	81	22	US-09-855-158-13	Sequence 13, Appl
9	201	100.0	181	22	US-09-854-864-5	Sequence 5, Appl
10	201	100.0	181	22	US-09-855-158-5	Sequence 5, Appl
11	201	100.0	184	1	PCT-US00-04665-1	Sequence 1, Appl
12	201	100.0	184	1	PCT-US00-04665-1	Sequence 1, Appl
13	201	100.0	184	1	PCT-US02-16106-47	Sequence 47, Appl
14	201	100.0	184	18	US-09-479-856-8	Sequence 8, Appl
15	201	100.0	184	19	US-09-565-423-11	Sequence 11, Appl
16	201	100.0	184	19	US-09-569-245-8	Sequence 8, Appl
17	201	100.0	184	20	US-09-627-206-8	Sequence 8, Appl
18	201	100.0	184	21	US-09-724-341-4	Sequence 1, Appl
19	201	100.0	184	23	US-09-914-119A-1	Sequence 1, Appl
20	201	100.0	184	24	US-10-068-063-7	Sequence 2, Appl
21	201	100.0	184	24	US-10-068-725-2	Sequence 2, Appl
22	201	100.0	184	24	US-10-077-137-1	Sequence 1, Appl
23	201	100.0	184	24	US-10-077-137-7	Sequence 7, Appl
24	201	100.0	184	24	US-10-077-438-1	Sequence 7, Appl
25	201	100.0	184	24	US-10-077-438-7	Sequence 7, Appl
26	201	100.0	184	25	US-10-115-192-8	Sequence 8, Appl
27	201	100.0	184	25	US-10-151-883-47	Sequence 27, Appl
28	201	100.0	184	25	US-10-152-363A-27	Sequence 27, Appl
29	201	100.0	184	27	US-09-215-688-8	Sequence 8, Appl
30	201	100.0	182	21	US-09-758-471-5100	Sequence 5100, Ap
31	201	100.0	182	26	US-10-235-953-5100	Sequence 5100, Ap
32	201	100.0	283	22	US-09-854-864-9	Sequence 9, Appl
33	201	100.0	283	22	US-09-855-158-9	Sequence 9, Appl
34	201	100.0	288	1	PCT-US02-06518-120	Sequence 120, App
35	201	100.0	302	25	US-10-115-192-12	Sequence 12, Appl
36	201	100.0	302	27	US-60-215-688-12	Sequence 12, Appl
37	201	100.0	207	24	US-10-077-137-3	Sequence 3, Appl
38	181	90.0	207	24	US-10-077-438-3	Sequence 3, Appl
39	136	67.7	185	1	PCT-US00-04665-2	Sequence 2, Appl
40	136	67.7	185	19	US-09-565-423-17	Sequence 17, Appl
41	136	67.7	185	22	US-09-854-864-11	Sequence 11, Appl
42	136	67.7	185	22	US-09-855-158-11	Sequence 11, Appl
43	136	67.7	185	23	US-09-914-119A-2	Sequence 2, Appl
44	136	67.7	185	23	US-09-914-119A-2	Sequence 2, Appl
45	136	67.7	281	22	US-09-854-864-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-7
Sequence 7, Application US/09854864
GENERAL INFORMATION: LARS EYDE
APPLICANT: TUI GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCNA,
FILE REFERENCE: A-686B
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 100.0%; Score 201; DB 22;
Best local similarity 100.0%; Pred. No. 8; 1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OR 1 CSONEYFSLHACIPCOLRCSNTPPLTCORYC 34
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Db 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 2

US-09-855-158-7

; Sequence 7, Application US/09855158
; GENERAL INFORMATION: LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, B
; FILE REFERENCE: A-686A
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match 100.0%; Score 201; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 8, 1e-17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

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Db 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 3

US-09-854-864-6

; Sequence 6, Application US/09854864
; GENERAL INFORMATION: LARS EYDE
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 100.0%; Score 201; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 1, 2e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

Db 5 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 38

RESULT 4

US-09-855-158-6

; Sequence 6, Application US/09855158
; GENERAL INFORMATION: LARS EYDE
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, B
; FILE REFERENCE: A-686A
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6

Query Match 100.0%; Score 201; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 1, 2e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

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Db 5 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 38

RESULT 5

US-09-854-864-21

; Sequence 21, Application US/09854864
; GENERAL INFORMATION: LARS EYDE
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 100.0%; Score 201; DB 22; Length 58;
Best Local Similarity 100.0%; Pred. No. 1, 3e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

Db 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 6

US-09-855-158-21

; Sequence 21, Application US/09855158
; GENERAL INFORMATION: LARS EYDE
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, B
; FILE REFERENCE: A-686A
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match 100.0%; Score 201; DB 22; Length 58;
Best Local Similarity 100.0%; Pred. No. 1, 3e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

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Db 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

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; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

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Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 7
US-09-854-864-13
; Sequence 13, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match          100.0%; Score 201; DB 22; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 8
US-09-855-158-13
; Sequence 13, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match          100.0%; Score 201; DB 22; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 9
US-09-854-864-5
; Sequence 5, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match          100.0%; Score 201; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 38

RESULT 10
US-09-855-158-5
; Sequence 5, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-5

Query Match          100.0%; Score 201; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 38

RESULT 11
US-09-855-158-13
; Sequence 13, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match          100.0%; Score 201; DB 22; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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PCT-US00-04665-1
; Sequence 1, Application PC/TUS00004665
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371W02
; CURRENT APPLICATION NUMBER: PCT/US00/04665
; CURRENT FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04665-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 12
PCT-US00-04925-1
; Sequence 1, Application PC/TUS00004925
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371W02
; CURRENT APPLICATION NUMBER: PCT/US00/04925
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04925-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US00-04665-1
; Sequence 1, Application PC/TUS00004665
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371W02
; CURRENT APPLICATION NUMBER: PCT/US00/04665
; CURRENT FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04665-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US00-04925-1
; Sequence 1, Application PC/TUS00004925
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371W02
; CURRENT APPLICATION NUMBER: PCT/US00/04925
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04925-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US00-16106-47
; Sequence 47, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
PCT-US00-16106-47

Query Match      100.0%; Score 201; DB 19; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US02-16106-47
; Sequence 11, Application US/09565423
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match      100.0%; Score 201; DB 19; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US02-16106-47
; Sequence 11, Application US/09565423
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match      100.0%; Score 201; DB 19; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
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-Tue Jan 7 10:36:58 2003

us-09-855-158-7.rapm

Page 5

Db 8 CSQNEYFDSLHACTPCQJRCSSNTPTLCQRYC 41

Search completed: January 7, 2003, 09:53:18
Job time : 57.0075 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 85.513 Seconds

(without alignments)
384,527 Million cell updates/sec

Title: US-09-855-158-6

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents, AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	284	100.0	51	22	US-09-855-158-6
3	284	100.0	181	22	US-09-854-864-5
4	284	100.0	181	22	US-09-855-158-5
5	284	100.0	184	1	PCT-US00-04665-1
6	284	100.0	184	1	PCT-US00-04925-1

7	284	100.0	184	1	PCT-US02-16106-47	Sequence 47, Appl
8	284	100.0	184	18	US-09-479-855-8	Sequence 8, Appl
9	284	100.0	184	19	US-09-565-423-11	Sequence 11, Appl
10	284	100.0	184	19	US-09-569-245-8	Sequence 8, Appl
11	284	100.0	184	20	US-09-627-206-8	Sequence 8, Appl
12	284	100.0	184	21	US-09-724-341-4	Sequence 4, Appl
13	284	100.0	184	23	US-09-914-119A-1	Sequence 1, Appl
14	284	100.0	184	24	US-10-008-063-7	Sequence 1, Appl
15	284	100.0	184	24	US-10-068-723-2	Sequence 1, Appl
16	284	100.0	184	24	US-10-077-137-1	Sequence 1, Appl
17	284	100.0	184	24	US-10-077-137-7	Sequence 1, Appl
18	284	100.0	184	24	US-10-077-438-1	Sequence 1, Appl
19	284	100.0	184	24	US-10-077-438-7	Sequence 1, Appl
20	284	100.0	184	25	US-10-115-192-8	Sequence 8, Appl
21	284	100.0	184	25	US-10-151-882-47	Sequence 47, Appl
22	284	100.0	184	25	US-10-152-363A-27	Sequence 27, Appl
23	284	100.0	184	27	US-60-215-688-8	Sequence 8, Appl
24	284	100.0	192	21	US-09-758-471-5100	Sequence 5100, Ap
25	284	100.0	192	26	US-10-235-953-5100	Sequence 5100, Ap
26	284	100.0	283	22	US-09-854-864-9	Sequence 9, Appl
27	284	100.0	283	22	US-09-855-158-9	Sequence 9, Appl
28	284	100.0	283	1	PCT-US02-06518-120	Sequence 120, App
29	270	95.1	302	25	US-10-115-192-12	Sequence 12, Appl
30	264	93.0	58	22	US-09-854-864-21	Sequence 21, Appl
31	264	93.0	58	22	US-09-855-158-21	Sequence 21, Appl
32	249	87.7	207	24	US-10-077-137-3	Sequence 3, Appl
33	249	87.7	207	24	US-10-077-438-3	Sequence 3, Appl
34	249	87.7	207	24	US-09-854-864-7	Sequence 7, Appl
35	201	70.8	34	22	US-09-854-864-7	Sequence 7, Appl
36	201	70.8	34	22	US-09-854-864-13	Sequence 13, Appl
37	201	70.8	81	22	US-09-854-864-13	Sequence 13, Appl
38	201	70.8	81	22	US-09-855-158-13	Sequence 13, Appl
39	186	65.5	185	1	PCT-US00-04665-2	Sequence 2, Appl
40	186	65.5	185	1	PCT-US00-04925-2	Sequence 2, Appl
41	186	65.5	185	19	US-09-565-423-17	Sequence 17, Appl
42	186	65.5	185	22	US-09-854-864-11	Sequence 11, Appl
43	186	65.5	185	22	US-09-855-158-11	Sequence 11, Appl
44	186	65.5	185	23	US-09-914-119A-2	Sequence 2, Appl
45	182	64.1	281	22	US-09-854-864-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-6
; Sequence 6, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AgP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

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Best local similarity 100.0%; Pred. No. 2.3e-25; Index 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 0;
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6

Query Match 100.0%; Score 284; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-854-864-5
; Sequence 5, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

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Best Local Similarity 100.0%; Pred. No. 7.5e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-855-158-5
; Sequence 5, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-5

Query Match 100.0%; Score 284; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 7.5e-25;
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; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371WO2
; CURRENT APPLICATION NUMBER: PCT/US00/04665
; CURRENT FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04665-1

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1, Application PC/TUS0004925
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371WO2
; CURRENT APPLICATION NUMBER: PCT/US00/04925
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
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PCT-US00-04925-1

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PCT-US02-16106-47
; Sequence 47, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; PRIOR FILING DATE: 2002-05-22
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16106-47

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RESULT 8

US-09-479-856-8
; Sequence 8, Application US/09479856
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75
; CURRENT APPLICATION NUMBER: US/09/479,856
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,068
; EARLIER FILING DATE: 1999-01-07
; EARLIER APPLICATION NUMBER: 60/169,890
; EARLIER FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-479-856-8

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RESULT 9

US-09-565-423-11

Sequence 11, Application US/09565423
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TAIL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

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Best Local Similarity 100.0%; Pred. No. 7,6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 MAGCCSONEYFDSLHACIPQOLRCSSNTPPLTCORYCNASVTNSVKGTNA 54

RESULT 10
US-09-569-245-8
; Sequence 8, Application US/09569245
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75
; CURRENT APPLICATION NUMBER: US/09/569,245
; PRIOR FILING DATE: 2000-05-11
; PRIOR FILING DATE: 1999-01-07
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 09/479,856
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-245-8

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Best Local Similarity 100.0%; Pred. No. 7,6e-25;
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RESULT 11
US-09-627-206-8
; Sequence 8, Application US/09627206
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: TAIL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-627-206-8

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Best Local Similarity 100.0%; Pred. No. 7,6e-25;
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RESULT 11
US-09-627-206-8
; Sequence 8, Application US/09627206
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: TAIL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-627-206-8

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; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75C2
; CURRENT APPLICATION NUMBER: US/09/627,206
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/569,245
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-627-206-8

Query Match      100.0%; Score 284; DB 20; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSNKGKGTNA 54

RESULT 12
US-09-724-341-4
; Sequence 4, Application US/09724341
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IGBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805E1
; CURRENT APPLICATION NUMBER: US/09/724,341
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-724-341-4

Query Match      100.0%; Score 284; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSNKGKGTNA 51
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSNKGKGTNA 54

RESULT 13
US-09-914-119A-1
; Sequence 1, Application US/09914119A
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian
; APPLICANT: Tsiang, Adrian
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; INTERMEDIATES
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; FILE REFERENCE: 00786/371002
; CURRENT APPLICATION NUMBER: US/09/914,119A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/04925
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/121,485
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-914-119A-1

Query Match      100.0%; Score 284; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSNKGKGTNA 51
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSNKGKGTNA 54

RESULT 14
US-10-008-063-7
; Sequence 7, Application US/10008063
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-008-063-7

Query Match      100.0%; Score 284; DB 24; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSNKGKGTNA 51
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSNKGKGTNA 54

RESULT 15
US-10-068-725-2
; Sequence 2, Application US/10068725
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-068-725-2
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Tue Jan 7 10:36:56 2003

us-09-855-158-6.rapm

Page 5

Query Match 100.0%; Score 284; DB 24; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAGCCSQQNEYPDSLHACIPQQLRCSSNTPPLTCORYCNASYTNSVKGTNA 51
Db 4 MAGCCSQQNEYPDSLHACIPQQLRCSSNTPPLTCORYCNASYTNSVKGTNA 54

Search completed: January 7, 2003, 09:53:18
Job time : 86.513 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:14 ; Search time 6.26316 Seconds
(without alignment)
239.587 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 1 MAGCCSQNEVFDLSLHACIP.....LTCRCYNASVTNSVKGTNA 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67.5	23.8	166	2	US-08-810-572A-6
2	67.5	23.8	166	4	US-09-290-333-6
3	67.5	23.8	293	2	US-08-810-572A-2
4	67.5	23.8	293	4	US-09-290-333-2
5	55.5	19.7	2476	2	US-08-276-967-2
6	55.5	19.5	5405	4	US-08-718-388-9
7	54.5	19.2	350	2	US-08-999-811-4
8	54.5	19.2	350	2	US-08-824-996-2
9	54.5	19.2	350	3	US-09-042-105-4
10	54.5	19.2	350	4	US-08-510-133A-3
11	54.5	19.2	350	4	US-08-585-895-33
12	54.5	19.2	419	2	US-08-999-811-2
13	54.5	19.2	419	3	US-09-042-105-2
14	54.5	19.2	419	3	US-09-042-105-18
15	54.5	19.2	419	4	US-08-795-430-8
16	54.5	19.2	419	4	US-08-510-133A-35
17	54.5	19.2	419	4	US-09-353-700-8
18	54.5	19.2	419	4	US-08-501-133-33
19	54.5	19.2	419	4	US-08-501-133-33
20	54.5	19.2	419	4	US-08-501-133-33
21	54.5	19.2	419	4	US-08-501-133-33
22	54.5	19.2	419	4	US-08-501-133-33
23	54.5	19.2	419	4	US-08-501-133-33
24	54.5	19.2	419	4	US-08-501-133-33
25	54.5	19.2	419	4	US-08-501-133-33
26	54.5	19.2	419	4	US-08-501-133-33
27	54.5	19.2	419	4	US-08-501-133-33

28	53.5	18.8	77	2	US-08-486-397-40	Sequence 40, Appl
29	53.5	18.8	77	2	US-08-486-399-4	Sequence 4, Appl
30	53.5	18.8	77	2	US-08-486-399-40	Sequence 40, Appl
31	53.5	18.8	77	2	US-08-461-965-4	Sequence 4, Appl
32	53.5	18.8	77	2	US-08-461-965-40	Sequence 40, Appl
33	53.5	18.8	77	2	US-08-326-110A-33	Sequence 33, Appl
34	53.5	18.8	77	2	US-08-634-641-4	Sequence 4, Appl
35	53.5	18.8	77	2	US-08-634-641-40	Sequence 40, Appl
36	53.5	18.8	77	3	US-09-249-471-4	Sequence 4, Appl
37	53.5	18.8	77	3	US-09-249-471-40	Sequence 40, Appl
38	53.5	18.8	77	3	US-09-249-472-4	Sequence 4, Appl
39	53.5	18.8	77	3	US-09-249-472-40	Sequence 40, Appl
40	53.5	18.8	77	3	US-09-249-451-4	Sequence 4, Appl
41	53.5	18.8	77	3	US-09-249-451-40	Sequence 40, Appl
42	53.5	18.8	77	3	US-08-809-455-4	Sequence 4, Appl
43	53.5	18.8	77	3	US-08-809-455-40	Sequence 40, Appl
44	53.5	18.8	77	3	US-09-249-461-4	Sequence 4, Appl
45	53.5	18.8	77	3	US-09-249-461-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYDROPHILIC: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: Homo sapiens
US-08-810-572A-6
Query Match 23.8%; Score 67.5; DB 2; Length 166;
Best local Similarity 30.6%; Pred. No. 0.64;


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Jackson Esq., David A.
;   REGISTRATION NUMBER: 26,742
;   REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-487-5800
;   TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 293 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match      23.8%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 1.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

OY      5  CSQNEVFDSLHACIPCOLRCSSNTPLTCORYCNA 40
DB      34  CPEQYWDPLGTGCMCKTICNMG-QRTCAFCRS 68

RESULT 5
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
;   APPLICANT: Hardy, Daniel M.
;   TITLE OF INVENTION: Specific-Egg-Binding Proteins of
;   TITLE OF INVENTION: Sperm
;   NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P. O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/276,967
;   FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kitchell, Barbara S.
;   REGISTRATION NUMBER: 33,928
;   REFERENCE/DOCKET NUMBER: UTSD:418\KIT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 713-787-1400
;   TELEFAX: 713-789-2679
;   TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2476 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-967-2
Query Match      19.7%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 2.6e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

OY      5  CSQNEVFDSLHACIP-CO---LRCSNTPLTCORYC 38
DB      1651  CSANSVTTCVPSCLPSCDPEGQCTGAGAPSTCEGC 1888

RESULT 6
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
;   APPLICANT: MORIKAWA, MINORU
;   TITLE OF INVENTION: GENE ENCODING I9G FC REGION-BINDING
;   TITLE OF INVENTION: PROTEIN
;   NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
;   STREET: PO BOX 747
;   CITY: FALLS CHURCH
;   STATE: VA
;   COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/718,388
;   FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
;   NAME: MURPHY JR, GERALD M
;   REGISTRATION NUMBER: 28,977
;   REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 205-8050
;   TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5405 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
; US-08-718-388-9
Query Match      19.5%; Score 55.5; DB 4; Length 5405;
Best Local Similarity 33.3%; Pred. No. 6.8e+02;
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2;

OY      4  QCSQNEVFDSLHACI-PQQLRCSSNTPLTCORYC 38
DB      3933  ECPDMSHTE---LCADTCSLGCSALAPLQCPDGC 3964

RESULT 7
US-08-999-811-4
; Sequence 4, Application US/08999811
; Patent No. 5932540
; GENERAL INFORMATION:
;   APPLICANT: HU, JING-SHAN
;   APPLICANT: ROSEN, CRAIG A.
;   APPLICANT: CAO, LIANG
;   TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;   NUMBER OF SEQUENCES: 15
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
;; STREET: 1100 NEW YORK AVENUE
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/999,811
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,550
;; FILING DATE: 8-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,968
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MARKOWICZ, KAREN R.
;; REGISTRATION NUMBER: 36,351
;; REFERENCE/DOCKET NUMBER: 1488.1000004
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-999-811-4

Query Match 19.2%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 8
US-824-996-2
;; Sequence 2, Application US/0824996B
;; Patent No. 5935820
;; GENERAL INFORMATION:
;; APPLICANT: Hu, Jing-Shan
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Cao, Liang
;; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
;; FILE REFERENCE: Pfl12D1
;; CURRENT APPLICATION NUMBER: US/08/824,996B
;; CURRENT FILING DATE: 1997-03-27
;; EARLIER APPLICATION NUMBER: 08/207,550
;; EARLIER FILING DATE: 1994-03-08
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 350
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;;
US-08-824-996-2

Query Match 19.2%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296
RESULT 9
US-09-042-105-4
;; Sequence 4, Application US/09042105
;; Patent No. 6040157
;; GENERAL INFORMATION:
;; APPLICANT: HU, JING-SHAN
;; APPLICANT: ROSEN, CRAIG A.
;; APPLICANT: CAO, LIANG
;; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
;; STREET: 1100 NEW YORK AVENUE
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/042,105
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,550
;; FILING DATE: 8-MAR-1994
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,968
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: TO BE ASSIGNED
;; FILING DATE: 24-DEC-1997
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ERIC K. STEFFE
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-09-042-105-4

Query Match 19.2%; Score 54.5; DB 3; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 10
US-08-510-133A-33
;; Sequence 33, Application US/08510133A
;; Patent No. 6221839
;; GENERAL INFORMATION:
;; APPLICANT: Alitalo, Kari

Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gaas, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-510-133A-33

Query Match 19.2%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 4 QCSONEYFDSLHACIPQOLRCSSNTP--PLTCORYCNAS 41
Db 258 QCGANREFDENTCQV-CKRTCPNOLNPGKCAECCTES 296

RESULT 11
US-08-585-895-33
Sequence 33, Application US/08585895
Patent No. 6245530
GENERAL INFORMATION:
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/585,895
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaas, David A.
REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28113/33072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-585-895-33

Query Match 19.2%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 4 QCSONEYFDSLHACIPQOLRCSSNTP--PLTCORYCNAS 41
Db 258 QCGANREFDENTCQV-CKRTCPNOLNPGKCAECCTES 296

RESULT 12
US-08-999-811-2
Sequence 2, Application US/08999811
Patent No. 5932540
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488,1000004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-999-811-2

Query Match 19.2%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 13
US-09-042-105-2
; Sequence 2, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2540
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-042-105-2

Query Match 19.2%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 14
US-09-042-105-18
; Sequence 18, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN

; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 18:
; LENGTH: 419 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-042-105-18

Query Match 19.2%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 15
US-08-795-430-8
; Sequence 8, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall,
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-430-8

Query Match 19.2%; Score 54.5; DB 4; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSQNEYFDSLHACIPQI RGSSTNP--PLTCQRYCNAS 41
DB 327 QCGANREFDENTQCV-CKRTCPRNQPLNPGKXACECTES 365

Search completed: January 7, 2003, 09:42:02
Job time : 8.26316 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 14.4436 Seconds
(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGCOSQNEYPDSLHACIP.....LTCORYCNASTNSVKGTNA 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74.5	26.2	966	5 Q22378	Q22378 caenorhabditis
2	72.5	25.5	499	11 Q88714	Q88714 mus musculus
3	71	25.0	532	5 O17496	O17496 ascaris suu
4	71	25.0	718	5 Q98107	Q98107 entamoeba h
5	69.5	24.5	5374	11 Q989D0	Q989D0 mus musculus
6	67	23.6	62	5 O77419	O77419 ascaris suu
7	66	23.2	330	5 O18118	O18118 caenorhabditis
8	65.5	23.1	548	5 Q9C045	Q9C045 giardia lam
9	65.5	23.1	1299	5 Q26489	Q26489 spodoptera
10	65	22.9	2551	4 Q88WQ8	Q88WQ8 homo sapien
11	63	22.2	175	11 Q8R4M8	Q8R4M8 mus musculus
12	63	22.2	341	11 Q9D351	Q9D351 mus musculus
13	62.5	22.0	999	5 Q17969	Q17969 caenorhabditis
14	62.5	22.0	1513	5 O17970	O17970 caenorhabditis
15	61.5	21.7	353	5 Q9VW81	Q9VW81 drosophila
16	61.5	21.7	353	5 Q8S258	Q8S258 drosophila

17	61.5	21.7	483	5 Q22423	Q22423 caenorhabditis
18	61	21.5	263	15 Q9WEJ8	Q9WEJ8 human immun
19	60.5	21.3	1574	11 Q88281	Q88281 rattus norv
20	60.5	21.3	3034	11 Q35161	Q35161 mus musculus
21	60	21.1	250	12 Q9DW27	Q9DW27 spodoptera
22	60	21.1	262	15 Q9WDX2	Q9WDX2 human immun
23	60	21.1	369	5 Q9VW90	Q9VW90 drosophila
24	60	21.1	387	13 Q9PVD4	Q9PVD4 xenopus lae
25	60	21.1	5146	6 Q8SPM4	Q8SPM4 bos taurus
26	59.5	21.0	856	10 Q945R4	Q945R4 hordeum vul
27	59	20.8	263	15 Q9WDU5	Q9WDU5 human immun
28	59	20.8	263	15 Q9WDU8	Q9WDU8 human immun
29	59	20.8	263	15 Q9WDV0	Q9WDV0 human immun
30	59	20.8	263	15 Q9WDV6	Q9WDV6 human immun
31	59	20.8	263	15 Q9WDV8	Q9WDV8 human immun
32	59	20.8	263	15 Q9WDV7	Q9WDV7 human immun
33	59	20.8	263	15 Q9WDW8	Q9WDW8 human immun
34	59	20.8	263	15 Q9WDW9	Q9WDW9 human immun
35	59	20.8	263	15 Q9WDX0	Q9WDX0 human immun
36	59	20.8	263	15 Q9WDX6	Q9WDX6 human immun
37	59	20.8	263	15 Q9WE18	Q9WE18 human immun
38	59	20.8	263	15 Q9WE19	Q9WE19 human immun
39	59	20.8	263	15 Q9WEJ0	Q9WEJ0 human immun
40	59	20.8	263	15 Q9WEJ1	Q9WEJ1 human immun
41	59	20.8	263	15 Q9WEJ2	Q9WEJ2 human immun
42	59	20.8	263	15 Q9WEJ4	Q9WEJ4 human immun
43	59	20.8	263	15 Q9WEJ5	Q9WEJ5 human immun
44	59	20.8	263	15 Q9WEJ7	Q9WEJ7 human immun
45	59	20.8	263	15 Q9WEJ9	Q9WEJ9 human immun

ALIGNMENTS

RESULT 1

Q22378 PRELIMINARY; PRT; 966 AA.
ID Q22378
AC Q22378
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 102.5 kDa protein.
GN T10E10.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RT Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Geisel C.;
RT "The sequence of C. elegans cosmid T10E10."
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct submission."
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; U36644; AAA80360.2; -.
DR HSSP; P10969; IMGT.
DR InterPro; IPR002557; Chitin_bind_PeRA.
DR InterPro; IPR000794; Ketoacyl-Synt.
DR InterPro; IPR003571; Snake_toxin.
DR InterPro; IPR002899; WRI/EB.

DR Pfam; PF01607; CBM_14; 2.
 DR SMART; SM00289; WRI; 12.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;
 Query Match 26.2%; Score 74.5; DB 5; Length 966;
 Best Local Similarity 36.7%; Pred. No. 0.048;
 Matches 18; Conservative 11; Mismatches 15; Indels 5; Gaps 3;
 QY 4 QCSQNEYFDSLHACIPQLR--CSSNTPPLTCQRYCNASVTSVKGTN 50
 Db 215 QCSQSTVFNSDLNVCVPLAIGNCSDSSTQDPVCS--C-SQVSSSCPQTS 260
 RESULT 2
 O88714 PRELIMINARY; PRT; 499 AA.
 AC O88714; 1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Gastric mucin-like protein (Fragment).
 GN GASTRIC MUCIN-LIKE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN R10 M.C.;
 RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
 RT "Identification of interactions between trefoil peptides and members
 of the mucin protein family using the yeast two-hybrid system.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ010752; CAA09343.1;
 DR HSP; P56682; ICCV
 DR InterPro; IPR002919; TIL_Cysrich.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF01826; TIL; 1.
 DR Pfam; PF00084; Vwd; 1.
 DR SMART; SM00216; VWD; 1.
 FT NON_TER 499 499
 SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EB61E CRC64;
 Query Match 25.5%; Score 72.5; DB 11; Length 499;
 Best Local Similarity 48.3%; Pred. No. 0.048; 7; Indels 7; Gaps 1;
 Matches 14; Conservative 1; Mismatches 7;
 QY 5 CSQNEYFDSLHACIPQLRCSNTPPLT 33
 Db 430 CSQNEYFDHSEGTGVCPC-----APPTT 451
 RESULT 3
 O17496 PRELIMINARY; PRT; 532 AA.
 AC O17496;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Serotonin receptor.
 OS Ascaris suum (big roundworm) (Ascaris lumbricoide),
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN R11
 RA SEQUENCE FROM N.A.
 RP MEDLINE=9939391; PubMed=10413046;
 RX Huang X., Duran E., Diaz F., Xiao H., Messer W.S. Jr., Komuniecki R.;

RT "Alternative-splicing of serotonin receptor isoforms in the pharynx
 RT and muscle of the parasitic nematode, Ascaris suum.";
 RL Mol. Biochem. Parasitol. 101:95-106(1999).
 DR EMBL; AF005486; AAC78396.1;
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 532 AA; 60140 MW; 4D795D1C249D55F6 CRC64;
 Query Match 25.0%; Score 71; DB 5; Length 532;
 Best Local Similarity 24.2%; Pred. No. 0.085;
 Matches 16; Conservative 14; Mismatches 16; Indels 20; Gaps 2;
 QY 1 MAGQCSQNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASVTS 45
 Db 435 MGVCKFGEYNSN-----VCSRNEFVLTDRQLDNVTISERPLLCGKHCSSGNS 489
 QY 46 VKGTNA 51
 Db 490 LQNNSA 495
 RESULT 4
 Q9BI07 PRELIMINARY; PRT; 718 AA.
 AC Q9BI07;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative cysteine surface protein (Fragment).
 GN CSP.
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN R11
 RA STRAIN-HMI; IMSS;
 RC MEDLINE=21428166; PubMed=11545438;
 RA Willhoest U., Campos-Gongora E., Fouzni S., Bruchhaus I., Tannich E.;
 RT "Introns of Entamoeba histolytica and Entamoeba dispar.";
 RL Proctist 152:149-156(2001).
 DR EMBL; AJ409106; CAC34072.1;
 DR InterPro; IPR002174; Furin-like.
 DR SMART; SM00261; FU; 7.
 FT NON_TER 718 718
 SQ SEQUENCE 718 AA; 80231 MW; FFF6362A49F2827A CRC64;
 Query Match 25.0%; Score 71; DB 5; Length 718;
 Best Local Similarity 27.1%; Pred. No. 0.11;
 Matches 13; Conservative 6; Mismatches 29; Indels 0; Gaps 0;
 QY 1 MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTSVK 48
 Db 137 LCGRCNDGSGYFDSTRTTCTCKCFNCELCSTSTNCFKCSNKILTESNG 184
 RESULT 5
 Q99ND0 PRELIMINARY; PRT; 5374 AA.
 AC Q99ND0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ZAN (Zonadhesin).
 GN ZAN
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN R11

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RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21138439; PubMed=11239002;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHF/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL Nucleic Acids Res. 29:1352-1365 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
RT "Genomic Basis of Inter- and Intra-species Variation in Zonahesin
RT Domain Structure.";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 3 MAM DOMAINS.
DR EMBL, AF312013, AK28824.1; -.
DR EMBL, AF040056, AL04416.1; -.
DR MGD, MGI:106566; Zm.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR000998; MAM_domain.
DR InterPro; IPR003328; TIL_Cyrich.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF00629; MAM; 3.
DR Pfam; PF01826; TIL; 25.
DR Pfam; PF02345; TILa; 25.
DR Pfam; PF00094; vwd; 4.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00274; FOLN; 21.
DR SMART; SM00137; MAM; 3.
DR SMART; SM00214; VWC; 25.
DR SMART; SM00216; VWD; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS00060; MAM_2; 3.
DR EGF-like domain; glycoprotein.
KM EGF-like domain; 5374 AA; 579536 MW; 90D2D8CF5B24EB CRC64;
SQ SEQUENCE 5374 AA; 579536 MW; 90D2D8CF5B24EB CRC64;

Query Match 24.5%; Score 69.5; DB 11; Length 5374;
Best Local Similarity 36.8%; Pred. No. 1.4;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 4 QCSQNEYPDSLHACIP-CQLRCSSNTP-PLTCQRYC 38
DB 3297 QCPNISOFTDCLPSCVPSNRCCEVSPSVSSCREGC 3334

RESULT 6
ID 077419 PRELIMINARY; PRT; 62 AA.
AC 077419;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chymotrypsin/elastase inhibitor-1 (Fragment).
GN ASC/-1
OS Aescaris suum (pig roundworm) (Ascaris lumbricoideae).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascarididae; Ascaris.
OC NCBI_Taxid=6253;
OX NCBI_Taxid=6253;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98297373; PubMed=9635450;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RA Anthrax simplex: mutational bursts in the reactive site centers of
RT serine protease inhibitors from an ascarid nematode.";
RL Exp. Parasitol. 89:257-261 (1998).
DR EMBL; U94499; AAC61300.1; -.
DR HSSP; P07851; IEAI.
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DR InterPro; IPR002919; TIL_Cyrich.
DR Pfam; PF01826; TIL; 1.
FT NON_TER 1
FT NON_TER 62
SQ SEQUENCE 62 AA; 6794 MW; 154CE25A375E0B2C CRC64;

Query Match 23.6%; Score 67; DB 5; Length 62;
Best Local Similarity 33.3%; Pred. No. 0.037;
Matches 17; Conservative 8; Mismatches 18; Indels 8; Gaps 4;

QY 4 QCSQNEYPDSLHACIPQQLRCS--SNTPLTCOR-YCNASYTNSVKGTN 50
DB 4 RCGNEVWTE---CTGCEMKCGDPENTPCPLMCRPRPCECSPGRWRRTN 50

RESULT 7
ID 018118 PRELIMINARY; PRT; 330 AA.
AC 018118;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE T33FL.6 protein.
GN T33FL.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; Z81129; CAB03405.1; -.
DR InterPro; IPR003341; DUF139.
DR Pfam; PF02363; DUF139; 7.
SQ SEQUENCE 330 AA; 36605 MW; F043B1A90DJA8FE9 CRC64;

Query Match 23.2%; Score 66; DB 5; Length 330;
Best Local Similarity 28.3%; Pred. No. 0.27;
Matches 15; Conservative 8; Mismatches 22; Indels 8; Gaps 2;

QY 5 CSQNEYPDSLHACIP-----CQLRCSSNTPPL--TCQRYCNASYTNSVKGT 49
DB 59 CASSQOQLQRTSCMPACQSCSQQCSQNTNTQCPTCQSCQSCQSCNPMST 111

RESULT 8
ID 09GQ45 PRELIMINARY; PRT; 548 AA.
AC 09GQ45;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Variant-specific surface protein M21-1 (Fragment).
GN M21-1.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OC NCBI_Taxid=5741;
OX NCBI_Taxid=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD-1;
RA Mansouri M., Ey P.L.;
RA A segment of a vsp12-like gene homolog from a type A-1 (group 1)
RT Giardia intestinalis isolate.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298862; AAG37862.1; -.
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DR HSP; P00136; 2CY3.
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR000545; CytC_heme_bind.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001174; Furin-like.
DR InterPro; IPR002350; kazal.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF-like; 1.
DR SMART; SM00261; FU; 5.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 548
SQ SEQUENCE 548 AA; 56557 MW; 578PE4FDA0A2CF0E CRC64;

Query Match 23.1%; Score 65.5; DB 5; Length 548;
Best Local Similarity 33.3%; Pred. No. 0.54;
Matches 19; Conservative 3; Mismatches 26; Indels 9; Gaps 3;

QY 2 AGCQSEYFDSLHACIPCOL----RCSSN---TPP--LTCQRYCNASVTNSVKGT 49
DB 209 AGCQDQGYADFTTGCKPCGTCATCEYNATISQCKTCSTSSNMVKTADGI 265

RESULT 9
Q26489 ID Q26489 PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Endoprotease furin.
GN FURIN.
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Noctuidae; Amphipyridae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SF9;
RA Clepik M.; Klenk H.;
RT "Cloning and functional characterization of FURIN from Spodoptera
RL frugiperda (SF9) cells."
RL Submitted (JAN1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68886; CAA3116.1; -.
DR HSP; Q99405; IMPI.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;

Query Match 23.1%; Score 65.5; DB 5; Length 1299;
Best Local Similarity 34.0%; Pred. No. 1.3;
Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

QY 5 CSQNEYFDSLHACIPCOLRCS-----SNTPTLTCQRYCNAS----VTNSVKG 48
DB 1150 CSRPLRLDRLNQCVCPC---CSRGVNTSPTPTDC-CHCNPENGECSNSVAG 1198

RESULT 10
Q8WQ8 ID Q8WQ8 PRELIMINARY; PRT; 2551 AA.
AC Q8WQ8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Stabilin-2.
GN STAB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Politz O.; Gratchev A.; McCourt P.A.G.; Schledzewski K.; Guillot P.;
RA Johanson S.; Birk R.; Hakiy N.; Franke P.; Kodelja V.; Kannicht C.;
RA Orfanos C.E.; Johanson S.; Goerd S.;
RT "Stabilin-1 and stabilin-2 constitute a novel family of fasciclin
RT domain-containing adhesion molecules associated with endothelial-
RT macrophage differentiation and angiogenic processes.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295695; CAC82105.1; -.
DR InterPro; IPR000782; BgH3_fasciclin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR000538; Link.
DR Pfam; PF00008; EGF; 20.
DR Pfam; PF02469; Fasciclin; 5.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00181; EGF; 24.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS00022; EGF 1; UNKNOWN 7.
DR PROSITE; PS01186; EGF 2; UNKNOWN 16.
DR PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN 2.
DR PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN 2.
SQ SEQUENCE 2551 AA; 276992 MW; 60A44651CC2BE59 CRC64;

Query Match 22.9%; Score 65; DB 4; Length 2551;
Best Local Similarity 30.0%; Pred. No. 3;
Matches 15; Conservative 4; Mismatches 9; Indels 22; Gaps 2;

QY 15 LHACIPCOL---RCSSNTPTPLT-----CORYCNASV 42
DB 674 LGTCVCSLVYNSRCFANSEPTALTRHCYVSGRFGSLKSGCARYCNATV 723

RESULT 11
Q8R4W8 ID Q8R4W8 PRELIMINARY; PRT; 175 AA.
AC Q8R4W8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRAF3 binding protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K.; Irie S.; Sato T.-A.;
RT "Identification of novel TRAF3 binding protein, T3BP, which increases
RT cellular p-actin content."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL63914.1; -.
DR PROSITE; PS00257; AAL63914.1; -.
SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EE93B1 CRC64;

Query Match 22.2%; Score 63; DB 11; Length 175;
Best Local Similarity 30.0%; Pred. No. 0.39;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 QCSQNEYFDSLHACIPCOL 23
DB 21 QCNQTECFDPLVRNCVSCCL 40

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RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de
RA Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fogle C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000)
DR EMBL; AE003114; AAF49068.1;
DR FlyBase; FBgn0016940; CG7148
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM_14; 4.
DR SMART; SM00494; ChEBD2; 3.
SQ SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;

Query Match 21.7%; Score 61.5; DB 5; Length 353;
Best Local Similarity 28.1%; Pred. No. 1.3;
Matches 16; Conservative 8; Mismatches 20; Indels 13; Gaps 3;

Qy 4 QCSQNEYFDSLHLHACIPCQL----RCSSNTP-----PLTCQRY--CNASVTNSVK 47
Db 118 KCSVGNVFPARRACLPVAISAHQCSCLVLPDNATLANPSCDCTYFRCHSGQAEVLQ 174

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Search completed: January 7, 2003, 09:40:03
Job time : 17.4436 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 3.83459 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGQCSQNEYFDLSLHACIP.....LTCGRYCNASVTSNKGKTN A 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	100.0	184	1	Q02223 homo sapien
2	186	65.5	185	1	TR17 MOUSE
3	71.5	25.2	249	1	TR13X MOUSE
4	70.5	24.8	1877	1	PKCS MOUSE
5	69.5	24.5	5376	1	ZAN MOUSE
6	67.5	23.8	293	1	TI3X HUMAN
7	66	23.2	63	1	ICEL ASCSU
8	63	22.2	175	1	TI3C MOUSE
9	62	21.8	1592	1	SORL CHICK
10	61.5	21.7	99	1	GAS3 ARATH
11	60.5	21.3	3034	1	CLRI MOUSE
12	60	21.1	1867	1	SSPO BOVIN
13	60	20.4	1816	1	LM44 MOUSE
14	58	20.1	1680	1	FUR2 DROME
15	57.5	20.2	708	1	YB40 HUMAN
16	57	20.1	1701	1	YAB5 SCHPO
17	56.5	19.9	701	1	ZAN PIC
18	56	19.7	2476	1	CATE RAT
19	55.5	19.5	3295	1	LM4E HUMAN
20	55.5	19.5	3695	1	CATR MOUSE
21	55	19.4	687	1	VS41 GALA
22	55	19.4	768	1	YJ06 YEAST
23	55	19.4	760	1	EZ DROME
24	54.5	19.2	419	1	VEEG HUMAN
25	54.5	19.2	532	1	TRN8 RAT
26	54.5	19.2	543	1	KPCZ MOUSE
27	54.5	19.0	1980	1	MY9B RAT
28	54	19.0	2114	1	MY9B MOUSE
29	54	19.0	2158	1	MY9B HUMAN
30	53.5	18.8	323	1	TNR8 BOVIN
31	53.5	18.8	325	1	VT2 SPVKA
32	53.5	18.8	381	1	P53 CANFA
33	53.5	18.8	381	1	P53 CANFA

34	53.5	18.8	1576	1	YLK3 CAEEL
35	53	18.7	131	1	ALX1 MOUSE
36	53	18.7	455	1	TR1A HUMAN
37	53	18.7	591	1	KPCZ RABIT
38	53	18.7	712	1	ENV HV22
39	53	18.7	859	1	ENV HV22
40	53	18.7	3075	1	LM41 HUMAN
41	52.5	18.5	495	1	TNR8 MOUSE
42	52.5	18.5	847	1	Y083 NPVAC
43	52.5	18.5	971	1	RECK MOUSE
44	52.5	18.5	3718	1	LM45 MOUSE
45	52	18.3	56	1	ITR4 RADMA

ALIGNMENTS

RESULT 1
ID TR17_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).
GN TNFRSF17 OR BCM4 OR BCM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Peripheral blood leukocytes, and lymph node;
RX MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a C (4,116) (G2C;P13) translocation in a malignant T cell lymphoma.";
RL EMO J. 11:3897-3904(1992).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94218235; PubMed=8165126;
RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "The BCM gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";
RL Nucleic Acids Res. 22:1147-1154(1994).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=9425270; PubMed=10493829;
RA Lotteus B.J., Kim U.-J., Shedd V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
[4]
RN SEQUENCE FROM N.A., AND VARIANT THR-153.
RX MEDLINE=21419161; PubMed=11528522;
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "presence of four major haplotypes in human BCM gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";
RL Genes Immun. 2:276-279(2001).
[5]
RN FUNCTION.
RP MEDLINE=20363816; PubMed=10903733;
RX Hatzoglu A., Roussel J., Bourgade M.-F., Rogier E., Madry C., Inoue J., Devygne O., Tsapis A.;
RT "TNF receptor family member BCM4 (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38

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RT RT mitogen-activated protein kinase.";
RL J. Immunol. 165:1322-1330(2000).
RP [6]
RX FUNCTION.
RX MEDLINE=20259066; PubMed=10801128;
RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
RA Madden J.A., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
RA Harrison K., Kindsvogel W., Clegg C.H.;
RA "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
RA autoimmune disease.";
RT Nature 404:995-999(2000).
RL [7]
RN FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
RP MEDLINE=21170294; PubMed=10973284;
RX Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Teitel L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
[8]
RN INTERACTION WITH TRAF5 AND TRAF6.
RP MEDLINE=20381353; PubMed=10908663;
RX Shu H.-B., Johnson H.;
RA "B cell maturation protein is a receptor for the tumor necrosis factor
RT family member TALL-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
CC Promotes B-cell survival and plays a role in the regulation of
CC humoral immunity. Activates NF-kappa-B and JNK.
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
CC and perinuclear Golgi-like structures.
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
CC cells of monocytosis.
CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
CC WHICH INVOLVES BCMA AND IL2.
CC -!- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC -----
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CC -----
DR EMBL; Z14954; CAA78679.1; -
DR EMBL; Z29575; CAA82691.1; -
DR EMBL; Z29574; CAA82690.1; -
DR EMBL; U95742; AAB67251.1; -
DR EMBL; AB052772; BAB60895.1; -
DR PIR; S31208;
DR PIR; S31209; S31209.
DR Genew; HGNC:11913; TNFRSF17.
DR MIM; 109545; -
KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
KW Transmembrane; Chromosomal translocation; Polymorphism.
FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 55 77 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT DOMAIN 78 184 CYTOPLASMIC (POTENTIAL).
FT REPEAT 7 41 TNFR-CYS.
FT SITE 3 4 BREAKPOINT FOR TRANSLOCATION TO FORM
FT INTERLEUKIN 2/BCM ONCOGENE.
FT DISULFID 8 21 BY SIMILARITY.
FT DISULFID 24 37 BY SIMILARITY.
FT DISULFID 28 41 BY SIMILARITY.
FT VARIANT 153 153 A -> T.
FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

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Query Match 100.0%; Score 284; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. NO. 2.7e-27;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTNA 51
DB 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGTNA 54
RESULT 2
TR17_MOUSE
ID TR17_MOUSE STANDARD; PRT; 185 AA.
AC 086472;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
DE maturation protein).
GN TNFRSF17 OR BCMA OR BCM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP STRAIN=BALB/C; TISSUE=Spleen;
RX MEDLINE=99061155; PubMed=9846698;
RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
RA Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
RT "The characterization of murine BCMA gene defines it as a new member
RT of the tumor necrosis factor receptor superfamily.";
RL Int. Immunol. 10:1693-1702(1998).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akasawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
CC Promotes B-cell survival and plays a role in the regulation of
CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms, 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
CC heart, and at lower levels in kidney and lung.
CC -!- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC -----
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DR EMBL; AF061505; AAC23799.1; -
 DR EMBL; AK020247; BAB32038.1; -
 DR MGI; MGI:1343050; TnfRsf17.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KM Alternative splicing.
 FT DOMAIN 1
 FT TRANSMEM 50 70
 FT REPEAT 71 185
 FT DISULFID 4 36
 FT DISULFID 5 18
 FT DISULFID 21 32
 FT DISULFID 25 36
 FT VARSPLIC 87 91
 FT SEQUENCE 185 AA; 20442 MW; 8806352B4FD20A8E CRC64;

Query Match
 Best Local Similarity 71.4%; Score 186; DB 1; Length 185;
 Matches 35; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 MAQCSENYFDSLHACTPQCRSSNTPPLTCORYCNASTNSVYKGT 49
 Db 1 MAQCSENYFDSLHACTPQCRSSNTPPLTCORYCNASTNSVYKGT 47

RESULT 3
 ID T13X MOUSE STANDARD; PRT; 249 AA.
 AC Q9ERT5; Q9DB23;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAMD interactor).
 GN TNFRSF13B OR TRAF1
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=21177254; PubMed=10881172;
 RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
 RT "Identification of a receptor for BLyS demonstrates a crucial role in humoral immunity";
 RL Nat. Immunol. 1:37-41(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=C57BL/6J; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi Y., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadono K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann M., Gasteigand T., Gissi C., King B., Kochina H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schmitt L.M., Stadhil F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Xing L., Furuno M., Aono H., Balcells R., Barsh G., Baker U., Bolleil D., Bojunga N., Carninci F., de Bonald M., Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M., Gustinich S., Hill D., Holman W., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Kombeerts P., Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Thall L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R., Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J., Meng S.-Y., Boyle W.J., Hsu H.;
 RT "TRAF1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis factor family member involved in B cell regulation";
 RL J. Exp. Med. 192:137-143(2000).
 [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TRAF1 and interactions are required for T cell activation and collagen-induced arthritis in mice";
 RL Nat. Immunol. 2:632-637(2001).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity (By similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLG with its C-terminus (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
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DR EMBL; AF257673; AAG00081.1; -
 DR EMBL; AK004668; BAB23457.1; -
 DR MGI; MGI:188941; TnfRsf13b.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1 128
 FT TRANSMEM 129 149
 FT REPEAT 150 249
 FT REPEAT 5 38
 FT DISULFID 6 19
 FT DISULFID 22 34
 FT DISULFID 26 38
 FT DISULFID 43 58
 FT DISULFID 61 72
 FT DISULFID 65 76
 FT CONFLICT 137 137
 FT SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match
 Best Local Similarity 25.2%; Score 71.5; DB 1; Length 249;
 Matches 12; Conservative 35.3%; Pred No 0.11; 13; Indels 1; Gaps 1;

Qy 5 CSQSENYFDSLHACTPQCRSSNTPPLTCORYC 38
 Db 6 CPKQDYMSRKSCVSCALTCORS-ORCTDFC 38

RESULT 4
 ID PKCS MOUSE STANDARD; PRT; 1877 AA.

AC Q04592; Q62040;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
 DE (Proprotein convertase PCS) (Subtilisin/kexin-like protease PCS)
 DE (Convertase PCS) (PC6) (Subtilisin-like proprotein convertase 6)
 DE (SPC6).
 GN PCSK5.
 OS Mus musculus (Mouse).
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID 10090;
 RN [1]
 RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
 RC STRAIN=ICR; TISSUE=Intestine;
 RA MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171(1993).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM PCSA).
 RP TISSUE=Brain, and Intestine;
 RC MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RL J. Biochem. 113:132-135(1993).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM PCSA).
 RP TISSUE=Adrenal cortex;
 RC MEDLINE=93342056; PubMed=8341687;
 RA Lussan J., Vieau D., Hamelin J.; Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [4]
 RN PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RP MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bendayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PC5 are sorted to different
 subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275(1996).
 RN [5]
 RN DEVELOPMENTAL EXPRESSION.
 RP MEDLINE=96293359; PubMed=8698813;
 RA Constam D.B., Calfon M., Robertson E.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 RN [6]
 RN DEVELOPMENTAL EXPRESSION.
 RP MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -1- FUNCTION LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 OF CLEAVAGE AT THE RX(N/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
 CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO

CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 CC EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PCSB/LONG (SHOWN HERE)
 CC AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 CC ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE
 CC INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 CC EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
 CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 CC E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 CC E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
 CC NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
 CC SAC FOLLOWED BY A CONFINEMENT TO DERMATOTOME COMPARTMENT. BETWEEN
 CC E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
 CC CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
 CC TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
 CC STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
 CC CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
 CC ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
 CC ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
 CC ISOFORM B OCCUR AT E12.5.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 CC SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 CC WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
 CC -----
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 CC -----
 CC EMBL; D17583; BAA04507.1; -;
 CC EMBL; D12619; BAA02143.1; -;
 CC EMBL; U14532; AAA74636.1; -;
 CC FIR; JX0248; JX0248.
 CC FIR; A48225; A48225.
 CC HSSP; Q99405; IMPT.
 CC MEROPS; S08.076; -;
 CC MGD; MGI:97515; Pcsk5.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR002174; Furin-like.
 CC InterPro; IPR002884; P_domain.
 CC InterPro; IPR002029; Peptidase_S8.
 CC Pfam; PF00082; Peptidase_S8; 1.
 CC Pfam; PF01483; P; PARTIAL.
 CC PRINTS; PR00723; SUBTILISIN.
 CC ProDom; PD000717; P_domain; 1.
 CC SMART; SM00181; EGF_3.
 CC SMART; SM00001; EGF_like; 2.
 CC SMART; SM00261; FU_22.
 CC PROSITE; PS00136; SUBTILASE ASP; 1.
 CC PROSITE; PS00137; SUBTILASE_HIS; 1.
 CC PROSITE; PS00138; SUBTILASE_SER; 1.
 CC Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
 CC Cleavage on pair of basic residues; Repeat; Alternative splicing;
 CC Transmembrane. 1 34
 CC SIGNAL 35 116
 CC PROPEP 117 1877
 CC CHAIN 117 1877
 CC PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
 CC TYPE 5.
 CC DOMAIN 117 1768
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 1769 1789
 CC POTENTIAL.
 CC DOMAIN 1790 1877
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 117 452
 CC CATALYTIC.
 CC DOMAIN 464 602
 CC HOMO B.


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FT DOMAIN 4264 4283 VFWD 20 (PARTIAL).
FT DOMAIN 4384 4503 VFWD 21 (PARTIAL).
FT DOMAIN 4504 4623 VFWD 22 (PARTIAL).
FT DOMAIN 4624 4743 VFWD 23 (PARTIAL).
FT DOMAIN 4744 4863 VFWD 24 (PARTIAL).
FT DOMAIN 4864 5295 VFWD 25.
FT DOMAIN 5259 5295 EGF-LIKE.
FT DIULFID 5263 5274 BY SIMILARITY.
FT DIULFID 5268 5283 BY SIMILARITY.
FT DIULFID 5285 5294 BY SIMILARITY.
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 492 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1216 1216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1239 1239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1314 1314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1814 1814 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1933 1933 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2028 2028 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2111 2111 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2142 2142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2332 2332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2575 2575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2692 2692 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2812 2812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3052 3052 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3065 3065 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3144 3144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3172 3172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3288 3288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3292 3292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3782 3782 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4005 4005 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4136 4136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4243 4243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4254 4254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4335 4335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4376 4376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4586 4586 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5136 5136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5252 5252 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 5376 AA; 57998 MW; 0B44DB7DF2A2620 CRC64;

Query Match 24.5%; Score 69.5; DB 1; Length 5376;
Best Local Similarity 36.8%; Pred. No. 3.4;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 4 QCSQNEYFDSLHACIP-COLRCSNTP--PLTCQRYC 38
Db 3299 QCPTNSQFTDCLPSCVPSGNCRCVTSFSPVSSCREGC 3336

RESULT 6
ID T13X HUMAN STANDARD; PRT; 293 AA.
AC O14836,
DT 15-JUN-2002 (Rel. 41, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U.; Bram R.J.;
SQ "NF-AT activation induced by a CAML-interacting member of the tumor

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RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Straubeberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=10956646; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Peng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinko D., Lafleur D.,
RA Misone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BLYS.";
RN J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RN Nat. Immunol. 1:252-256(2000).
CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein.
CC interesting and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF023614; AAC51790.1; -
CC EMBL; BC028072; AAH28072.1; -
CC Genew; HGNC:18153; TNFRSF13B.
CC MIM; 604907; -
CC
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS0050; TNFR_NGFR_2; FALSE NEG.
CC Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Repeat.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT DOMAIN 187 293 CYTOPLASMIC (POTENTIAL).
FT REPEAT 33 67 TNFR-CYS 1.
FT REPEAT 70 104 TNFR-CYS 2.
FT DISULFID 34 47 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 251 251 P -> L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

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Query Match      23.8%; Score 67.5; DB 1; Length 293;
Best Local Similarity 30.6%; Pred. No. 0.38;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

OY 5 CSQNEYFDSLHACIPQRCSSNTPLPTLCORYCNA 40
   34 CPEQYWDPLGTGCMSCKTCIKNHOS-QRTCAFCRS 68

RESULT 7
ID ICE1_ASCSU STANDARD; PRT; 63 AA.
AC P07851;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chymotrypsin/elastase isoinhibitor 1 (C/E-1 inhibitor).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=84255715; PubMed=6564898;
RA Babin D.R., Peanasky R.J., Goos S.M.;
RT "The isoinhibitors of chymotrypsin/elastase from Ascaris
RT lumbricoidea: the primary structure."
RL Arch. Biochem. Biophys. 232:143-161(1984).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
RP MEDLINE=95060335; PubMed=7922044;
RA Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;
RT "The molecular structure of the complex of Ascaris
RT chymotrypsin/elastase inhibitor with porcine elastase."
RL Structure 2:679-689(1994).
CC -1- FUNCTIONALITY: BELONGS TO THE ORGANISM AGAINST THE HOST'S PROTEINASES.
CC -1- SIMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.
DR PIR: S07127; S07127.
DR PDB: 1EAI; 05-APR-99.
DR Interpro: IPR002919; TIL_Cysrich.
DR Pfam: PF01826; TIL: 1.
DR Serni: Protease inhibitor; 3d-structure.
FT DISULFID 5 38
FT DISULFID 14 33
FT DISULFID 17 29
FT DISULFID 21 60
FT DISULFID 40 54
FT ACT SITE 31 32
SQ SEQUENCE 63 AA; 6862 MW; 5DC1DE75B375F16 CRC64;

Query Match      23.2%; Score 66; DB 1; Length 63;
Best Local Similarity 34.0%; Pred. No. 0.14;
Matches 17; Conservative 7; Mismatches 18; Indels 8; Gaps 4;

OY 5 CSQNEYFDSLHACIPQRC--SSNTP-PLTCOR-YCNASVTNSVKGTN 50
   5 CGNEVWTE---CTGCEMKKCGPDENTPCPLMCRPSCSCSPGRGMRRTN 50

RESULT 8
ID T13C_MOUSE STANDARD; PRT; 175 AA.
AC Q9P8D0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
DE 3) (B-cell maturation defect).
GN TNFRSF13C OR BAFFR OR BCMD OR BR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BALB/C; TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Teschop J., Browning J.L.,
RA Ambrose C.;
RT "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF."
RL Science 293:2108-2111(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RC STRAIN=A/J;
RX MEDLINE=21475520; PubMed=11591325;
RA Yan M., Brady T.R., Chan B.I., Lee W.P., Hau B., Harless S.M.,
RA Cancro M.P., Grewal I.S., Dixie V.M.;
RT "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency."
RL Curr. Biol. 11:1547-1552(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush T.,
RA Schirral L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Wang G.,
RA Blake K., Ostfeld D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [4]
RP FUNCTION.
RX MEDLINE=2161654; PubMed=11747827;
RA Harless S.M., Lentz V.M., Sah A.P., Heu B.L., Clise-Dwyer K.,
RA Hilbert D.M., Hayes C.E., Cancro M.P.;
RT "Competition for Blys-mediated signaling through Bcmd/BR3 regulates
RT peripheral B lymphocyte numbers."
RL Curr. Biol. 11:1986-1989(2001).
CC -1- FUNCTION: B-cell receptor specific for TNFRSF13B/TAL1/BAFF/Blys.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
CC detected at lower levels in lung and thymus.
CC -1- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell
CC deficiency B-cell deficient strain A/WySnJ has a 4.7 kb insertion
CC in the BAFF gene leading to an altered C-terminus. The mutant RNA
CC is not detectable. B-cell lymphoprolasts is normal, but the life
CC span of peripheral B-cells is much reduced.
CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC -----
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CC -----
DR EMBL; AF373847; AK91827.1; -.
DR EMBL; AK008142; BAB25490.1; -.
DR MGI; MGI:191299; Tnfrsf13c.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
FT FT 72 92 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT FT 93 175 CYTOPLASMIC (POTENTIAL).
FT FT REPEAT 21 38 TNFR-CYS (PARTIAL).
FT FT REPEAT 22 35 BY SIMILARITY.
FT FT DTSULFID 27 38 BY SIMILARITY.
FT FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT VARSPLIC 133 143 MISSING (IN ISOFORM 2).
FT FT SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;
Query Match 22.2%; Score 63; DB 1; Length 175;
Best Local Similarity 50.0%; Pred. No. 0.81;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 4 QCSNEYFDSLLHACIPCOL 23
DB 21 QCNQTECFDLVNCVSCEL 40
RESULT 9
ID -SORL_CHICK STANDARD; PRT; 1592 AA.
AC Q98930;
AT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sortilin-related receptor (Sorting protein-related receptor containing
DE LDLR class A repeats) (SorLA) (SorLA-1) (Low-density lipoprotein
DE receptor relative with 11 ligand-binding repeats) (LDLR relative with
DE 11 ligand-binding repeats) (LR11) (Fragment).
OS Gallus gallus (Chicken)
OC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97301565; PubMed=9157966;
RA Moriwaki S., Yamazaki H., Bujo H., Kusunoki J., Kanaki T., Seimiya K.,
RA Moriwaki N., Nimpf J., Schneider W.J., Saito Y.;
RT "A novel mosaic protein containing LDL receptor elements is highly
RT conserved in humans and chickens."
RL Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).
CC -1- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT
CC MAY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEINS AND OF PROTEASES.
CC BINDS LDL, THE MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA,
CC AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS. BINDS THE RECEPTOR-
CC ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL
CC INTERACTION. BOTH ESTROGEN STATUS AND CHOLESTEROL LEVELS LACK
CC REGULATORY EFFECTS ON THIS RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN. PRESENT IN THE
CC TESTES, ADRENAL GLANDS AND DETECTABLE IN THE LUNG.
CC -1- SIMILARITY: CONTAINS 5 BNR REPEATS.
CC -1- SIMILARITY: CONTAINS 11 LDL-RECEPTOR CLASS A DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL; Y08109; CAA69324.1; -.
DR HSSP; P01130; IAUJ.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR002860; GH_BNR.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00057; ldl_recept_a; 11.
DR Pfam; PF00058; ldl_recept_b; 5.
DR Pfam; PF02012; BNR; 5.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00192; LDLa; 11.
DR SMART; SM00135; LY; 5.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01209; LDLA_1; 11.
DR PROSITE; PS00068; LDLRA_2; 11.
KW Endocytosis; Receptor; EGF-like domain; Repeat; Glycoprotein; LDL;
KW Lipid transport; Cholesterol metabolism.
FT NON_TER 1 1
FT REPEAT 43 54 BNR 1.
FT REPEAT 139 150 BNR 2.
FT REPEAT 348 359 BNR 3.
FT REPEAT 428 439 BNR 4.
FT REPEAT 469 480 BNR 5.
FT DOMAIN 710 884 5 X APPROXIMATE YWTD REPEATS.
FT REPEAT 710 713 1.
FT REPEAT 754 757 2.
FT REPEAT 798 801 3.
FT REPEAT 841 844 4.
FT REPEAT 881 884 5.
FT DOMAIN 933 979 EGF-LIKE.
FT DOMAIN 1021 1021 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 1022 1062 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 1063 1100 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 1103 1143 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 1143 1180 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 1180 1224 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 1230 1268 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 1273 1312 LDL-RECEPTOR CLASS A 8.
FT DOMAIN 1324 1362 LDL-RECEPTOR CLASS A 9.
FT DOMAIN 1376 1415 LDL-RECEPTOR CLASS A 10.
FT DOMAIN 1419 1457 FIBRONECTIN TYPE-III 1.
FT DOMAIN 1462 1551 FIBRONECTIN TYPE-III 1.
FT DOMAIN 1559 >1592 FIBRONECTIN TYPE-III 2.
FT DISULFID 985 997 BY SIMILARITY.
FT DISULFID 992 1010 BY SIMILARITY.
FT DISULFID 1004 1019 BY SIMILARITY.
FT DISULFID 1024 1038 BY SIMILARITY.
FT DISULFID 1032 1051 BY SIMILARITY.
FT DISULFID 1045 1060 BY SIMILARITY.
FT DISULFID 1065 1077 BY SIMILARITY.
FT DISULFID 1072 1090 BY SIMILARITY.
FT DISULFID 1084 1099 BY SIMILARITY.
FT DISULFID 1105 1117 BY SIMILARITY.
FT DISULFID 1112 1130 BY SIMILARITY.
FT DISULFID 1124 1141 BY SIMILARITY.
FT DISULFID 1145 1158 BY SIMILARITY.
FT DISULFID 1150 1168 BY SIMILARITY.
FT DISULFID 1162 1222 BY SIMILARITY.
FT DISULFID 1232 1244 BY SIMILARITY.
FT DISULFID 1239 1257 BY SIMILARITY.
FT DISULFID 1261 1266 BY SIMILARITY.
FT DISULFID 1275 1288 BY SIMILARITY.
FT DISULFID 1283 1301 BY SIMILARITY.
FT DISULFID 1295 1310 BY SIMILARITY.
FT DISULFID 1333 1351 BY SIMILARITY.
FT DISULFID 1345 1360 BY SIMILARITY.
FT CARBOHYD 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 6
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FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 778 778 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 975 975 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1098 1098 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1152 1152 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1366 1366 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1454 1454 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1514 1514 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT NON_TER 1592 1592 N-LINKED (GLCNAC. . .) (POTENTIAL)
SO SEQUENCE 1592 AA; 178409 MW; 24EDDA5BA231B203 CRC64;

Query Match 21.8%; Score 62; DB 1; Length 1592;
Best Local Similarity 33.3%; Pred. No. 8.6;
Matches 15; Conservative 6; Mismatches 18; Indels 6; Gaps 2;

Cy 3 GGCSONEYFDSLHACIP---COLF-CSSNTPPLTCQRYCNAS 41
Db 1376 GRCSTRFECQOLHKCIPMKRCDCGRDCCDGTDRSCPTHSLS 1420

RESULT 10
ID GAS3_ARATH STANDARD; PRT; 99 AA.
AC G46687;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gibberellin-regulated protein 3 precursor.
GN GAS3 OR AT4G09600 OR T25P22.40.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Ericales; Brassicales; Brassicaceae; Arabidopsids.
CC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Seed;
RX MEDLINE=95244835; PubMed=7727751;
RA Herzog M., Dorner A.-M., Grellet F.;
RT "GAS3, a gibberellin-regulated gene family from Arabidopsis thaliana
RT related to the tomato GAS1 gene."
RL Plant Mol. Biol. 27:743-752(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Scheller C., Wandt R., Murphy G., Volckaert G.,
RA Pohl T., Dueserhoef A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Heidegger M., de Simone V., Obermaier B., Mache R., Weiler M.,
RA Kreis M., Delany M., Putz-Enders P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohenseil J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bigham L., Robben J., Vandenbusche F.,
RA van der Schueren U., Gironprez B., Chuang I.-O., Vandenbusche F.,
RA Breken W., Melijns I., Voet M., Baetians I., Aert K., Defoor E.,
RA Welzenberger I., Botne G., Ramepeter U., Hilbert H., Braun M.,
RA Moollan P., Klein Lankhorst R., Rose M., Hauf J., Koeller P.,
RA Bernier S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA de Keyser A., Buysaert C., Gielen J., Villarroel R., Van Cleve R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McAlay K., Mayes R.,
RA Pectet A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fatmann B., Granderath K., Danner D., Herzl A.,
RA Neumann S., Argitrou A., Vitale D., Ligouri R., Piravandi E.,

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RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Punelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heinen L., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bayan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dehry N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalkick J., Graves T., Harmon G., Edwards J.,
RA Letrelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer U., Fulton L., Mardis E., Dante M., Pepin K., Hiller L.,
RA Nelson U., Spiech U., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali U., Bergtholt A., Jones K., Drome K., Cotton W., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hamed A., Loch M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777(1999).
CC -1- FUNCTION: INVOLVED IN LATE STAGES OF SEED MATURATION, OR IN EARLY
CC STEPS OF GERMINATION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: SILIQUES AND DRY SEEDS.
CC -1- PTM: SIX DISULFIDE BONDS MAY BE PRESENT.
CC -1- SIMILARITY: BELONGS TO THE GAS1 FAMILY.
CC -----
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DR EMBL; U11764; AAB06308.1; -
DR EMBL; AL161515; CAB78083.1; -
DR EMBL; AL161831; CAB82127.1; -
DR InterPro; IPR003854; GAS3.
DR Pfam; PF02704; GAS3.1.
KW Multigene family; Signal.
FT SIGNAL 1 18
FT CHAIN 19 99 GIBBERELLIN-REGULATED PROTEIN 3.
FT SEQUENCE 99 AA; 10704 MW; 84549B74B08A47FA CRC64;
SO SEQUENCE FROM N.A.

Query Match 21.7%; Score 61.5; DB 1; Length 99;
Best Local Similarity 35.6%; Pred. No. 0.72;
Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;

Cy 3 GGCSONEYFDSLHACIPCOLRCSSNTPPLTCQRY---CNASVT 43
Db 47 GRCSSSRPVLCLRACNSCCYRCNC-VPRPTAGNHHLCPYASIT 90

RESULT 11
ID CLRL_MOUSE STANDARD; PRT; 3034 AA.
AC O3516;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cadherin EGF Lag seven-pass G-type receptor 1 precursor.
GN CERS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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FT DISULFID 1668 1679 BY SIMILARITY.
FT DISULFID 1673 1688 BY SIMILARITY.
FT DISULFID 1690 1699 BY SIMILARITY.
FT DISULFID 1891 1902 BY SIMILARITY.
FT DISULFID 1896 1911 BY SIMILARITY.
FT DISULFID 1913 1922 BY SIMILARITY.
FT DISULFID 1926 1937 BY SIMILARITY.
FT DISULFID 1931 1949 BY SIMILARITY.
FT DISULFID 1951 1960 BY SIMILARITY.
FT DISULFID 1960 1978 BY SIMILARITY.
FT DISULFID 1968 1981 BY SIMILARITY.
FT DISULFID 2000 2015 BY SIMILARITY.
FT DISULFID 2020 2036 BY SIMILARITY.
FT DISULFID 2020 2036 BY SIMILARITY.
FT MOD_RES 1681 1681 BY SIMILARITY.
FT MOD_RES 1904 1904 HYDROXYLATION (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 793 793 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1129 1129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1154 1154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1228 1228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1264 1264 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1274 1274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1302 1302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1591 1591 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1638 1638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1655 1655 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1994 1994 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2118 2118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2137 2137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2144 2144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2155 2155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2160 2160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2272 2272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2430 2430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2452 2452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2538 2538 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 3034 AA; 330477 MW; 8FF38180AF5ED8A8 CRC64;

Query Match 21.3%; Score 60.5; DB 1; Length 3034;
Best Local Similarity 28.3%; Pred. No. 24;
Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;

QY 4 QCSQNEFYFLHACIPCOL-----RCSNTPLTQ-----RYCN-----ASVTN 44
Db 2001 QCSQNEFYFLHACIPCOL-----RCSNTPLTQ-----RYCN-----ASVTN 44

RESULT 12
SSPO BOVIN STANDARD; PRT; 867 AA.
AC P98167;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE SCO-spondin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_taxid=9913;
RX TISSUE=ependymocyte;
RX MEDLINE=96338614; PubMed=8743952;
RA Gobion S., Monnerie H., Meinzel R., Creveaux I., Lehmann W.,
RA Lamalle D., Dastugue B., Meinzel A.;
RT "SCO-spondin: a new member of the thrombospondin family secreted by
RT the subcommissural organ is a candidate in the modulation of neuronal
RT aggregation.";
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RL J. Cell Sci. 109:1053-1061(1996).
CC -1- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
CC -1- DEVELOPMENTAL STAGE: EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC -1- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X93922; CA63815.1; -.
DR HSBP; P01130; IAUJ.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR002919; TIL_Cysrich.
DR InterPro; IPR000884; TSP1.
DR Pfam; PFO0057; ldl_recept_a; 3.
DR Pfam; PFO0093; tsp_1; 4.
DR Pfam; PFO0093; tsc_1.
DR Pfam; PFO0754; F5_P8_type_C; 1.
DR Pfam; PFO1826; TIL; 1.
DR SMART; SM00192; LDCA; 3.
DR SMART; SM00192; FA58C; 1.
DR SMART; SM00209; TSP1; 4.
DR SMART; SM00214; VMC; 1.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01285; FA58C_2; 1.
DR PROSITE; PS01208; LDLRA_1; 3.
DR PROSITE; PS50068; LDLRA_2; 3.
DR PROSITE; PS50092; TSP1; 4.
KM Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
FT NON_TER 1 1
FT DOMAIN 26 81 TSP TYPE-1.
FT DOMAIN 103 142 EGF-LIKE 1.
FT DOMAIN 143 180 EGF-LIKE 2.
FT DOMAIN 185 243 TSP TYPE-1 2.
FT DOMAIN 344 502 F5/8 TYPE C.
FT DOMAIN 506 544 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 663 701 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 723 761 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 762 813 TSP TYPE-1 3.
FT DOMAIN 814 867 TSP TYPE-1 4.
FT DISULFID 107 122 BY SIMILARITY.
FT DISULFID 116 127 BY SIMILARITY.
FT DISULFID 129 141 BY SIMILARITY.
FT DISULFID 147 166 BY SIMILARITY.
FT DISULFID 149 179 BY SIMILARITY.
FT DISULFID 171 179 BY SIMILARITY.
FT DISULFID 344 502 BY SIMILARITY.
FT DISULFID 508 520 BY SIMILARITY.
FT DISULFID 515 530 BY SIMILARITY.
FT DISULFID 527 542 BY SIMILARITY.
FT DISULFID 665 677 BY SIMILARITY.
FT DISULFID 672 690 BY SIMILARITY.
FT DISULFID 684 699 BY SIMILARITY.
FT DISULFID 725 737 BY SIMILARITY.
FT DISULFID 732 750 BY SIMILARITY.
FT DISULFID 744 759 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 867 867
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;
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FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 550 550 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 751 751 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 780 780 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 803 803 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1283 1283 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1361 1361 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CONFLICT 8 8 C -> S (IN REF. 2)
FT CONFLICT 18 18 C -> Y (IN REF. 2)
FT CONFLICT 248 248 C -> R (IN REF. 3)
FT CONFLICT 297 297 G -> A (IN REF. 3)
FT CONFLICT 431 431 THR -> HPS (IN REF. 2)
FT CONFLICT 679 679 S -> C (IN REF. 3)
FT CONFLICT 703 703 D -> G (IN REF. 2)
FT CONFLICT 706 706 N -> H (IN REF. 2)
FT CONFLICT 728 728 K -> R (IN REF. 2)
FT CONFLICT 730 730 F -> I (IN REF. 2)
FT CONFLICT 779 779 R -> G (IN REF. 1)
FT CONFLICT 810 810 R -> S (IN REF. 3)
FT CONFLICT 865 865 ASP -> QT (IN REF. 2)
FT CONFLICT 936 936 K -> E (IN REF. 3)
FT CONFLICT 970 970 L -> V (IN REF. 3)
FT CONFLICT 1132 1132 H -> R (IN REF. 2)
FT CONFLICT 1200 1200 F -> I (IN REF. 2)
FT CONFLICT 1382 1382 D -> A (IN REF. 2)
FT CONFLICT 1413 1414 NS -> EF (IN REF. 1)
FT CONFLICT 1489 1489 A -> S (IN REF. 2)
SQ SEQUENCE 1816 AA; 201818 MW; B49C45F3A45999D8 CRC64;

Query Match 21.1%; Score 60; DB 1; Length 1816;
Best local Similarity 23.8%; Pred. No. 17;
Matches 15; Conservative 10; Mismatches 22; Indels 16; Gaps 2;

QY 2 AGCCGNEVDSILHACIPQ-----LRCSNTPPLTCQRYCNASTNSV 46
DB 64 AERCDAG-FRRTUSGECAPCDGNGSHCLDGGFCLHCORNTGHCERKCLDGYIGDSI 122
QY 47 KGT 49
DB 123 RGT 125

RESULT 14
LMA4_HUMAN
ID LMA4_HUMAN STANDARD; PRT; 1816 AA.
AC Q16363; Q15335; Q14735; Q9UE18; Q9UUN9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-4 chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart; PubMed=9310354;
RX MEDLINE=97454279; PubMed=9310354;
RA Richards A.J., Lucchini C., Pope F.M.;
RT "The structural organisation of LMA4, the gene encoding laminin
alpha4.";
RL Eur. J. Biochem. 248:15-23(1997).
RP [3]
RP SEQUENCE OF 236-1816 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=9504381; PubMed=7959779;
RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA Pope F.M.;
RT "Localization of the gene (LMA4) to chromosome 6q21 and isolation of
RT a partial cDNA encoding a variant laminin A chain.";
RL Genomics 22:237-239(1994).
RP [4]
RP SEQUENCE OF 66-1816 FROM N.A.
RA Tubbey B.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANE (MAJOR COMPONENT).
CC -1- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG,
CC OVARY SMALL, AND LARGE INTESTINES, PLACENTA, LIVER; WEAK OR NO
CC EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANCREAS, TESTIS, PROSTATE,
CC BRAIN. HIGH EXPRESSION IN FETAL LUNG AND KIDNEY. EXPRESSION IN
CC FETAL AND NEWBORN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS
CC IN TISSUES SUCH AS SMOOTH MUSCLE AND DERMIS.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS 1 AND 11 ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN 5 IS GLOBULAR.
CC -1- SIMILARITY: CONTAINS 3.5 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC -1- CAUTION: GENE LMA4 WAS FORMERLY CALLED LMA3.
CC -----
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CC -----
CC EMBL; S78569; AAB34635.1; -
CC EMBL; X91171; CA62596.1; -
CC EMBL; Y14240; CA47436.1; -
CC EMBL; X76939; CA54258.1; -
CC EMBL; Z99289; CAB16553.1; -
CC HSSP; P02468; IKLO.
CC Genew; HGNC:6484; LMA4.
CC MIM; 600133; -
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR002045; Laminin-EGF.
CC InterPro; IPR001791; Laminin-G.
CC Pfam; PF00054; Laminin-EGF; 6.
CC Pfam; SM00180; EGF_Lam; 5.
CC SMART; SM00282; LamG; 5.
CC PROSITE; PS00022; EGF_1; UNKNOWN_1.
CC PROSITE; PS01248; LAMININ_TYRE_EGF; 3.
CC PROSITE; PS50025; LAM_G_DOMAIN; 5.
CC GlycoProtein; Basement membrane; Extracellular matrix; Coiled coil;
CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97454279; PubMed=9310354;
RA Richards A.J., Lucchini C., Pope F.M.;
RT "The structural organisation of LMA4, the gene encoding laminin
alpha4.";
RL Eur. J. Biochem. 248:15-23(1997).
RP [3]
RP SEQUENCE OF 236-1816 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=9504381; PubMed=7959779;
RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA Pope F.M.;
RT "Localization of the gene (LMA4) to chromosome 6q21 and isolation of
RT a partial cDNA encoding a variant laminin A chain.";
RL Genomics 22:237-239(1994).
RP [4]
RP SEQUENCE OF 66-1816 FROM N.A.
RA Tubbey B.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANE (MAJOR COMPONENT).
CC -1- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG,
CC OVARY SMALL, AND LARGE INTESTINES, PLACENTA, LIVER; WEAK OR NO
CC EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANCREAS, TESTIS, PROSTATE,
CC BRAIN. HIGH EXPRESSION IN FETAL LUNG AND KIDNEY. EXPRESSION IN
CC FETAL AND NEWBORN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS
CC IN TISSUES SUCH AS SMOOTH MUSCLE AND DERMIS.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS 1 AND 11 ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
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CC -1- SIMILARITY: CONTAINS 3.5 LAMININ G-LIKE DOMAINS.
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CC -----
CC EMBL; S78569; AAB34635.1; -
CC EMBL; X91171; CA62596.1; -
CC EMBL; Y14240; CA47436.1; -
CC EMBL; X76939; CA54258.1; -
CC EMBL; Z99289; CAB16553.1; -
CC HSSP; P02468; IKLO.
CC Genew; HGNC:6484; LMA4.
CC MIM; 600133; -
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR002045; Laminin-EGF.
CC InterPro; IPR001791; Laminin-G.
CC Pfam; PF00054; Laminin-EGF; 6.
CC Pfam; SM00180; EGF_Lam; 5.
CC SMART; SM00282; LamG; 5.
CC PROSITE; PS00022; EGF_1; UNKNOWN_1.
CC PROSITE; PS01248; LAMININ_TYRE_EGF; 3.
CC PROSITE; PS50025; LAM_G_DOMAIN; 5.
CC GlycoProtein; Basement membrane; Extracellular matrix; Coiled coil;
CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

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OM protein - protein search, using BW model

Run on: January 7, 2003, 09:40:20 : Search time 3.83459 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGCSONEYFDSLHACIP.....LTCORCNASVYNSVKGTTNA 51

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	284	100.0	51	10	US-09-854-864-6	Sequence 6, Appl1
2	284	100.0	181	10	US-09-854-864-5	Sequence 5, Appl1
3	284	100.0	184	9	US-10-077-438-1	Sequence 1, Appl1
4	284	100.0	184	9	US-10-077-438-7	Sequence 7, Appl1
5	284	100.0	184	9	US-10-077-137-1	Sequence 1, Appl1
6	284	100.0	184	9	US-10-077-137-7	Sequence 7, Appl1
7	284	100.0	283	10	US-09-854-864-9	Sequence 9, Appl1
8	264	93.0	58	10	US-09-854-864-21	Sequence 21, Appl1
9	249	87.7	207	9	US-10-077-438-3	Sequence 3, Appl1
10	249	87.7	207	9	US-10-077-137-3	Sequence 3, Appl1
11	201	70.8	34	10	US-09-854-864-7	Sequence 7, Appl1
12	201	70.8	81	10	US-09-854-864-13	Sequence 13, Appl1
13	186	65.5	185	10	US-09-854-864-11	Sequence 11, Appl1
14	182	64.1	281	10	US-09-854-864-10	Sequence 10, Appl1
15	109	38.4	117	10	US-09-854-864-12	Sequence 12, Appl1
16	67.5	23.8	37	9	US-09-779-050A-45	Sequence 45, Appl1
17	67.5	23.8	59	10	US-09-854-864-20	Sequence 20, Appl1
18	67.5	23.8	166	10	US-09-854-864-15	Sequence 15, Appl1
19	67.5	23.8	291	9	US-09-779-050A-43	Sequence 43, Appl1

20	67.5	23.8	293	9	US-09-779-050A-42	Sequence 42, Appl
21	67.5	23.8	293	9	US-10-084-971-2	Sequence 2, Appl
22	67.5	23.8	293	10	US-09-879-919-22	Sequence 22, Appl
23	67.5	23.8	293	10	US-09-854-864-14	Sequence 14, Appl
24	67.5	23.8	293	10	US-09-961-376-2	Sequence 2, Appl
25	67.5	23.8	293	10	US-09-854-864-18	Sequence 18, Appl
26	66.5	23.4	67	10	US-09-854-864-16	Sequence 16, Appl
27	65.5	23.1	788	12	US-10-078-928-152	Sequence 15, App
28	64.5	22.7	418	9	US-09-886-429-2	Sequence 2, Appl
29	64.5	22.7	735	10	US-09-898-570-12	Sequence 10, Appl
30	64.5	22.7	845	10	US-09-898-570-12	Sequence 12, Appl
31	64.5	22.7	974	10	US-09-898-570-14	Sequence 14, Appl
32	64.5	22.7	1009	10	US-09-898-570-16	Sequence 16, Appl
33	61.5	21.7	99	9	US-09-950-933A-82	Sequence 82, Appl
34	60.5	21.3	3034	10	US-09-737-149-30	Sequence 25, Appl
35	60.5	21.3	3034	10	US-09-737-149-30	Sequence 46, Appl
36	59	20.8	38	9	US-09-779-050A-46	Sequence 10, Appl
37	58	20.4	162	10	US-09-798-789-10	Sequence 15, Appl
38	55.5	19.5	132	10	US-09-840-795-15	Sequence 116, App
39	55.5	19.5	870	12	US-10-078-928-188	Sequence 116, App
40	55.5	19.5	5405	9	US-10-025-380-1116	Sequence 359, App
41	55.5	19.5	5405	10	US-09-922-217-1116	Sequence 2, Appl
42	55	19.4	524	9	US-10-108-605-359	Sequence 3, Appl
43	54.5	19.2	350	9	US-10-060-523-2	Sequence 12, Appl
44	54.5	19.2	419	9	US-10-044-622-3	
45	54.5	19.2	419	9	US-09-852-209A-12	

ALIGNMENTS

RESULT 1
US-09-854-864-6
Sequence 6, Application US/09854864
Parent No. US2002081296A1
GENERAL INFORMATION: LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLVS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854, 864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 100.0% Score 284; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MAGCSONEYFDSLHACIPQALRCSSNTPTLCORCNASVYNSVKGTTNA 51
Db 1 MAGCSONEYFDSLHACIPQALRCSSNTPTLCORCNASVYNSVKGTTNA 51

RESULT 2
US-09-854-864-5
Sequence 5, Application US/09854864
Parent No. US2002081296A1
GENERAL INFORMATION: LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLVS/AGP-3, AND TACI

```
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      100.0%; Score 284; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
Db 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51

RESULT 3
US-10-077-438-1
; Sequence 1, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match      100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 54

RESULT 4
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
```

```
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 54

RESULT 5
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

Query Match      100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 54
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RESULT 6

US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US2002017674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Schnepf, Jurgen
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Balf Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match

Best Local Similarity 100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 51

Db 4 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 54

RESULT 7

US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-864-9

Query Match

Best Local Similarity 100.0%; Score 284; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 1,9e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 51
Db 1 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 51

RESULT 8

US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-864-21

Query Match

Best Local Similarity 93.0%; Score 264; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 5,6e-22;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CSQNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 51

Db 1 CSQNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 47

RESULT 9

US-10-077-438-3
; Sequence 3, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Schnepf, Jurgen
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Balf Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

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Best Local Similarity 87.7%; Score 249; DB 9; Length 207;
Best Local Similarity 70.6%; Pred. No. 7,4e-20;
Matches 48; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Qy 1 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 40
Db 1 MAGCCSNEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTA 40


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Oy      1 MAGCCSÖNEYFDLSLHACIPCÖLRCSNTPLTCÖRYCNASVTVSKGT 49
        ||| : ||| ||| ||| : ||| : ||| : |||
Db      1 MAQCÖFHSEYFDLSLHACKPCHLRCSN--PPATCÖPYCDPSVTVSKGT 47

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```

RESULT 14
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, IARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
TITLE OF INVENTION: BLYS/AGP-3, AND TAC1
FILE REFERENCE: A-686B
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US/09/854, 864
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 281
TYPE: PRT
ORGANISM: Mus musculus
US-09-854-864-10

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	Query Match Similarity	64.1%	Score 183	DB 10	Length 281;
	Best Local Similarity	69.4%	Pred. No. 1,3e-12;		
	Matches	34;	Conservative	5;	Mismatches 8; Indels 2; Gaps 1,
OY	1 MAGCCGNGRFFDILLACTPCCQRCGSNNRPILTCOCYACNASTVNSKGT	49			
	:				
	: :: :				
	: :: :				
	: :: :				
	: :: :				
DB	1 MAOQCCHSEYFDLLHACKCPHLNCSS--PPATCPCYCDSSTVSISKGS	47			

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RESULT 15
US-09-854-864-12
: Sequence 12, Application US/09854864
: Patent No. US20020081296A1
: GENERAL INFORMATION:
: APPLICANT: THEILL, LARS EYDE
: APPLICANT: YU, GANG
: TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
: TITLE OF INVENTION: BLYS/AGP-3, AND TACI
: FILE REFERENCE: A-686B
: CURRENT APPLICATION NUMBER: US/09/854,864
: CURRENT FILING DATE: 2001-09-11
: PRIOR APPLICATION NUMBER: US 60/204,039
: PRIOR FILING DATE: 2000-05-12
: PRIOR APPLICATION NUMBER: US 60/214,591
: PRIOR FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 12
: LENGTH: 117
: TYPE: PRT
: ORGANISM: human-murine Consensus
US-09-854-864-12

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Query Match	38.4%	Score 109	DB 10	Length 117
Best Local Similarity	70.5%	Pred. No. 3.3e-05		
Matches 31	Conservative 1	Mismatches 2	Indels 10	Gaps 6

OY	6	SQNEYFDSILHACTIPCOLRGSSNNPILTCORYCYMASTNSVKTG	49
Db	2	AQCEYFDSLHAC-PC-LRCS---PFTQ-YC-SVT-SVKTG	35

Search completed: January 7, 2003, 09:54:53
Job time : 3.83459 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:39 ; Search time 18.2782 Seconds
(without alignment) 371.797 Million cell updates/sec

Title: US-09-855-158-6
Perfect score: 284
Sequence: 1 MAGOCSQNEFYDSLHACIP.....ITCRPCNAYSVNKGKTN A 51

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: A_Geneseq_101002.*
 - 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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 - 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 24: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	100.0	51	AAE15485	Human B-cell matur
2	284	100.0	181	AAE15484	Human B-cell matur
3	284	100.0	184	AAE15483	Human B-cell matur
4	284	100.0	184	AAE15482	Human B-cell matur
5	284	100.0	184	AAE15481	Human B-cell matur
6	284	100.0	184	AAE15480	Human B-cell matur
7	284	100.0	184	AAE15479	Human B-cell matur
8	284	100.0	184	AAE15478	Human B-cell matur
9	284	100.0	184	AAE15477	Human B-cell matur
10	284	100.0	184	AAE15476	Human B-cell matur

11	270	95.1	302	AAE00507	Human BCMA-Immunog
12	270	95.1	302	AAE00506	Human BCMA-Immunog
13	264	93.0	58	AAE15501	Human B cell matur
14	264	93.0	58	AAE15500	Human B cell matur
15	201.5	71.0	157	AAE15486	Human B cell matur
16	186	65.5	185	AAE15485	Human B cell matur
17	186	65.5	185	AAE15484	Human B cell matur
18	186	65.5	185	AAE15483	Human B cell matur
19	182	64.1	181	AAE15482	Human B cell matur
20	109	38.4	217	AAE15491	Human BCMA-human 1
21	90.5	31.9	24	AAE15492	Human-murine BCMA
22	71.5	25.2	249	AAE15493	A murine znf14, a
23	67.5	23.8	37	AAE15500	Human AGP-3 recept
24	67.5	23.8	59	AAE15501	Human TACI cyto
25	67.5	23.8	166	AAE15494	Human TACI cyto
26	67.5	23.8	166	AAE15495	Human TACI cyto
27	67.5	23.8	265	AAE15496	Human TACI cyto
28	67.5	23.8	265	AAE15497	Human TACI cyto
29	67.5	23.8	265	AAE15498	Human TACI cyto
30	67.5	23.8	265	AAE15499	Human TACI cyto
31	67.5	23.8	265	AAE15500	Human TACI cyto
32	67.5	23.8	265	AAE15501	Human TACI cyto
33	67.5	23.8	265	AAE15502	Human TACI cyto
34	67.5	23.8	265	AAE15503	Human TACI cyto
35	67.5	23.8	265	AAE15504	Human TACI cyto
36	67.5	23.8	265	AAE15505	Human TACI cyto
37	67.5	23.8	265	AAE15506	Human TACI cyto
38	67.5	23.8	265	AAE15507	Human TACI cyto
39	67.5	23.8	265	AAE15508	Human TACI cyto
40	67.5	23.8	265	AAE15509	Human TACI cyto
41	67.5	23.8	265	AAE15510	Human TACI cyto
42	67.5	23.8	265	AAE15511	Human TACI cyto
43	67.5	23.8	265	AAE15512	Human TACI cyto
44	67.5	23.8	265	AAE15513	Human TACI cyto
45	66.5	23.4	33	AAE15495	Human TACI cyto

ALIGNMENTS

RESULT 1
AAE15485
ID AAE15485 standard; peptide; 51 AA.
XX
AC AAE15485;
XX
12-MAR-2002 (first entry)
XX
Human B-cell maturation (BCMA) protein extracellular domain.
XX
Human; transmembrane activator and intracellular CAML interactor; TACI,
XX
cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX
lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX
prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX
drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX
Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX
rheumatoid arthritis; atherosclerosis.
XX
Homo sapiens.
XX
PN WO200187979-A2.
XX
22-NOV-2001.
XX
14-MAY-2001; 2001WO-US15567.
XX
12-MAY-2000; 2000US-204039P.
XX
27-JUN-2000; 2000US-214591P.
XX
14-MAY-2001; 2001US-0214591.
XX
(AMGE-) AMGEN INC.

PI Theill LE, Yu G;
 XX WPI; 2002-066686/09.
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 XX Claim 1; Fig 10A; 94pp; English.
 PS
 XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein extracellular domain.
 XX
 XX Sequence 51 AA;
 QQ
 Query Match 100.0%; Score 284; DB 23; Length 51;
 Best Local Similarity 100.0%; Pred No. 8.3e-27;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
 DB 1 MAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
 RESULT 2
 AAE15484
 ID AAE15484 standard; Protein; 181 AA.
 XX
 XX AAE15484;
 XX
 XX 12-MAR-2002 (first entry)
 XX
 XX Human B-cell maturation (BCMA) protein.
 XX
 XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 5..38
 FT /note= "Cysteine-rich consensus region; This is region
 FT is specifically claimed as SEQ ID NO: 7 in claim 1 of
 FT the specification"
 FT 52..72
 FT Domain /label= Transmembrane_domain
 FT
 XX WO200187979-A2.
 XX

PD 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US15567.
 XX
 XX 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Theill LE, Yu G;
 PI
 XX WPI; 2002-066686/09.
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 XX Disclosure; Fig 10A; 94pp; English.
 PS
 XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein.
 XX
 XX Sequence 181 AA;
 QQ
 Query Match 100.0%; Score 284; DB 23; Length 181;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
 DB 1 MAGCQSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
 RESULT 3
 AAB08843
 ID AAB08843 standard; peptide; 184 AA.
 XX
 XX AAB08843;
 XX
 XX 02-JAN-2001 (first entry)
 XX
 XX Amino acid sequence of human.
 XX
 XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Domain 57..77
 FT /note= "putative transmembrane domain"
 FT
 XX WO2000050633-A1.
 XX

XX 31-AUG-2000.
PD 24-FEB-2000; 2000MO-US04925.
XX 24-FEB-1999; 99US-0121485.
XX (GENO) GEN HOSPITAL CORP.
XX Seed B, Ting A;
XX WPI; 2000-558405/51.
XX
XX Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
XX gene and reporter gene, and determining alteration in reporter gene
XX expression
XX
XX Claim 32; Fig 7A; 53pp; English.
XX
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA
XX is a necrosis factor (NF)-kB activator. The method of the invention is
XX used to identify compounds which modulate BCMA activity (and thus NF-kB
XX activity). The specification describes a method of identifying a
XX polypeptide which increases gene expression from a promoter. The method
XX involves contacting a library of with a cell which expresses a
XX recombinant anti-cell death gene and a reporter gene operably linked to
XX the promoter, and then determining whether the expression of the
XX reporter gene is altered as a result of contact with library. The method
XX is useful for identifying polypeptides which increase or decrease gene
XX expression from a promoter. The BCMA polypeptide or nucleic acid are
XX useful for preparing a pharmaceutical composition for treating cancer,
XX arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
XX identifying compounds that modulate NF-kB expression and thus for drug
XX designing.
XX
XX Sequence 184 AA:
SQ
Query Match 100.0%; Score 284; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGCCSNEYFDLSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 51
DB 4 MAGCCSNEYFDLSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 54
RESULT 4
AA094001
ID AA094001 standard; Protein; 184 AA.
XX
XX AA094001;
AC
XX 20-OCT-2000 (first entry)
DT
XX
XX A human BCMA protein, a B cell protein related to TACI.
DE
XX Human, BR3x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumor necrosis factor; TNF;
XX zntf4 activity; antibody production; autoimmune disease; amyloidosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX renal stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
XX Homo sapiens.
OS
XX
XX WO200040716-A2.
PN
XX

XX 13-JUL-2000.
PD 07-JAN-2000; 2000MO-US00396.
XX 07-JAN-1999; 99US-0226533.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX WPI; 2000-452538/39.
XX N-PSDB; AA58559.
XX
XX Inhibiting zntf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR3x2, TACI or BCMA extracellular domain polypeptide -
XX
XX Disclosure; Page 152; 175pp; English.
XX
XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumor necrosis factor (TNF) receptor. The extracellular
XX domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for used
XX for inhibiting zntf4 activity. Zntf4 is a TNF ligand. They may also be used
XX for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
XX with activated or resting B lymphocytes, effector T-cells, or with
XX antibody production. The antibody production is associated with an
XX autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis and rheumatoid arthritis. The zntf4 activity
XX and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
XX asthma, bronchitis, emphysema, end stage renal failure,
XX glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
XX amyloidosis, multiple myelomas, lymphomas, light chain neuropathy,
XX rejection, graft versus host disease, immunosuppression, graft
XX diabetes mellitus, Crohn's disease, inflammation, insulin dependent
XX septic shock, BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
XX agonists or antagonists can be used to treat hypertension, renal artery
XX stenosis, or occlusion, and cholesterol or renal emboli.
XX
XX Sequence 184 AA:
SQ
Query Match 100.0%; Score 284; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGCCSNEYFDLSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 51
DB 4 MAGCCSNEYFDLSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 54
RESULT 5
AAE09241
ID AAE09241 standard; Protein; 184 AA.
XX
XX AAE09241;
AC
XX 19-NOV-2001 (first entry)
DT
XX
XX Human BCMA protein.
DE
XX Human; TNF; tumor necrosis factor; TALL-1; APRIL; TNF receptor;
XX TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis;
XX psoriasis.
XX
XX Homo sapiens.
OS
XX
XX WO200160397-A1.
PN
XX
XX 23-AUG-2001.
PD

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XX PF 28-NOV-2000; 2000WO-US32378.
XX PR 16-FEB-2000; 2000US-0182938.
XX PR 22-AUG-2000; 2000US-0226986.
XX PA (GETH ) GENENTECH INC.
XX AS Aghkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
XX PI Yan M;
XX DR WPI; 2001-541628/60.
XX DR N-PSDB; AAD15902.
XX PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
XX PT activity, for treating autoimmune disorders and cancer, comprises
XX PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
XX PT antagonists.
XX EX Example 2; Fig 2; 160pp; English.
XX CC The invention relates to methods of using one or more agonists or
XX CC antagonists to modulate the activity of the members of TNF (tumour
XX CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
XX CC e.g. TACI or BCMA. The method is useful for treating pathological
XX CC conditions or diseases associated with increased TALL-1 and APRIL
XX CC expression or activity. TALL-1 and APRIL antagonists are used to
XX CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
XX CC They are useful for treating a mammal suffering from cancer such
XX CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
XX CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
XX CC psoriasis and lupus erythematosus. The present sequence is human
XX CC BCMA protein.
XX SQ Sequence 184 AA;
XX
Query Match 100.0%; Score 284; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3,3e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGQCSNEYFDSLHACIPCOLRCSNTPTLTQRYCNASVTSVKGTNA 51
DB 4 MAGQCSNEYFDSLHACIPCOLRCSNTPTLTQRYCNASVTSVKGTNA 54
RESULT 6
AAE00506
ID AAE00506 standard; Protein; 184 AA.
XX AC AAE00506;
XX DT 31-JUL-2001 (first entry)
XX DE Human B cell maturation protein (BCMA).
XX KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX KW organ transplantation; HIV; human immunodeficiency virus; TNF;
XX KW tumour necrosis factor; BCMA; B cell maturation protein.
XX OS Homo sapiens.
XX FN WO200124811-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27579.
XX PR 06-OCT-1999; 99US-0157933.
XX PR 11-FEB-2000; 2000US-0181807.

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PR 30-JUN-2000; 2000US-0215688.
XX (BIOJ ) BIOGEN INC.
XX PA (APOT-) APOTEC R & D SA.
XX PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX DR WPI; 2001-266242/27.
XX DR N-PSDB; AAD03844.
XX PT Treating a mammal for a condition associated with undesired cell
XX PT proliferation such as cancer or carcinoma, comprises administering a
XX PT composition comprising A Proliferation Inducing Ligand Receptor
XX PT (APRIL-R) antagonist.
XX PS Claim 3; Fig 3A; 85pp; English.
XX CC The invention relates to a method of treating a mammal for a condition
XX CC associated with undesired cell proliferation such as cancer or
XX CC carcinoma. The method involves administering a composition comprising
XX CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
XX CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX CC interaction between APRIL and its cognate receptor(s). This method is
XX CC useful for treating undesired cell proliferation such as cancer or
XX CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX CC prostate carcinoma, and other carcinomas whose proliferation is modulated
XX CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX CC diseases, renal disorders, B-cell lympho-proliferative disorders,
XX CC immunosuppressive diseases, organ transplantation, inflammation and
XX CC human immunodeficiency virus (HIV), and for treating, suppressing or
XX CC altering an immune response involving a signalling pathway between
XX CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
XX CC The present sequence is human APRIL-R also referred as BCMA or
XX CC BCM protein.
XX SQ Sequence 184 AA;
XX
Query Match 100.0%; Score 284; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3,3e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGQCSNEYFDSLHACIPCOLRCSNTPTLTQRYCNASVTSVKGTNA 51
DB 4 MAGQCSNEYFDSLHACIPCOLRCSNTPTLTQRYCNASVTSVKGTNA 54
RESULT 7
AAB60698
ID AAB60698 standard; Protein; 184 AA.
XX AC AAB60698;
XX DT 22-MAY-2001 (first entry)
XX DE Human BAFF receptor (BAFF-R).
XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX KW immune-related disorder; B-cell growth inhibitor; BCMA;
XX KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX KW renal disorder; immunosuppressive disorder; HIV infection;
XX KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX KW lymphoma; gene therapy; cancer; tumour.
XX OS Homo sapiens.
XX FN WO200112812-A2.
XX PD 22-FEB-2001.

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PF 16-AUG-2000; 2000WO-US22507.
 XX
 PR 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX
 PA (BIOI) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 PI Thompson J;
 DR WPI; 2001-202866/20.
 DR N-PSDB; AAF5998.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAF-R-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAF-R
 PT antibody homolog -
 XX
 PS Claim 20; Fig 1; 59pp; English.
 XX
 CC The invention relates to the use of a BAF-R receptor (BAF-R, also known
 CC as BCMA) protein, or a BAF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAF-R, fusion proteins containing it, and BAF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders. B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAF-R
 CC proteins or BAF-R specific antibodies may be used for treating
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAF-R.
 CC
 SQ Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 284; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.3e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MAGGCSQNEVFPSLHACIPQCLRCSSNTPLTCORVCNASTVTSVKGTA 51
 DB 4 MAGGCSQNEVFPSLHACIPQCLRCSSNTPLTCORVCNASTVTSVKGTA 54
 XX
 RESULT 8
 AAY71979 standard; Protein: 184 AA.
 ID AAY71979;
 AC AAY71979;
 XX
 DT 28-MAR-2001 (first entry)
 DE Human B cell maturation factor (BCMA) protein.
 XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMa;

KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..62
 FT /label= Extracellular_domain
 XX
 PN MO200068378-A1.
 XX
 PD 16-NOV-2000.
 XX
 PE 05-MAY-2000; 2000WO-US12266.
 PR 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Shu HS;
 PI WPI; 2001-016094/02.
 DR N-PSDB; AAD02125.
 XX
 PT Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 PS Claim 37; Page 104-105; 112pp; English.
 XX
 CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related Leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16. In human tissues, BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.
 CC
 SQ Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 284; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.3e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MAGGCSQNEVFPSLHACIPQCLRCSSNTPLTCORVCNASTVTSVKGTA 51
 DB 4 MAGGCSQNEVFPSLHACIPQCLRCSSNTPLTCORVCNASTVTSVKGTA 54
 XX
 RESULT 9
 ABB81487
 ID ABB81487 standard; Protein: 184 AA.
 AC ABB81487;
 XX
 DT 02-SEP-2002 (first entry)
 DE Human B cell maturation factor (BCMA) protein.
 XX

DE XX Human BCMA receptor related protein SEQ ID NO:7.

KW Human; Ztnfr12; tumour necrosis factor receptor; cytotostatic; immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritis; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pylonelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.

KW Homo sapiens.

OS Homo sapiens.

PN WO200238766-A2.

XX 16-MAY-2002.

PF 05-NOV-2001; 2001WO-US47018.

XX 07-NOV-2000; 2000US-246449P.

PR 20-DEC-2000; 2000US-257131P.

PR 28-JUN-2001; 2001US-301715P.

PR 29-AUG-2001; 2001US-315565P.

XX (ZYMO) ZYMOGENETICS INC.

PA Gross JA, Xu W, Henne RM, Grant FJ;

PI WPI; 2002-508212/54.

DR Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.

XX Disclosure; Page 135-136; 154pp; English.

PS The present invention describes a human tumour necrosis factor receptor designated Ztnfr12 (I) (I) has cytotostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, antirheumatic, antiarthritis, antiasthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. Ztnf4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pylonelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention.

XX Sequence 184 AA;

SQ Query Match 100.0%; Score 284; DB 23; Length 184; Best Local Similarity 100.0%; Pred. No. 3.3e-26; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCQNEYPFDSLHACIFCQLRCSNTPLTCQRYCNASVTNSVKGNTA 51

DB 4 MAGCQNEYPFDSLHACIFCQLRCSNTPLTCQRYCNASVTNSVKGNTA 54

RESULT 10

ID AAE15488 standard; Protein; 283 AA.

XX AAE15488;

AC 12-MAR-2002 (first entry)

DT Human BCMA-immunoglobulin Fc region fusion protein.

DE Human; transmembrane activator and intracellular CAML interactor; TAC1; cytotostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein.

XX Homo sapiens.

OS Homo sapiens.

PN WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US15567.

XX 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

PR 14-MAY-2001; 2001US-0214591.

XX (AMGE-) AMGEN INC.

PA Theill LE, Yu G;

PI WPI; 2002-066686/09.

DR Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumour necrosis factor family ligand.

XX Disclosure; Fig 10B; 94pp; English.

PS The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1 and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect stinging allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein.

XX Sequence 283 AA;

SQ Query Match 100.0%; Score 284; DB 23; Length 283; Best Local Similarity 100.0%; Pred. No. 5.1e-26; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCQNEYPFDSLHACIFCQLRCSNTPLTCQRYCNASVTNSVKGNTA 51

DB 1 MAGCQNEYPFDSLHACIFCQLRCSNTPLTCQRYCNASVTNSVKGNTA 51

ID	AAE00507	standard; Protein; 302 AA.
XX	AAE00507;	
XX	31-JUL-2001	(first entry)
XX		
DE	Human BCMA-Immunoglobulin G Fc region fusion construct.	
XX	Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;	
XX	gene therapy; cancer; nephrotoxic; renal disorder; autoimmune disease;	
KW	carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;	
KW	systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;	
KW	B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;	
KW	organ transplantation; HIV; human immunodeficiency virus; TYP; murine;	
KW	tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;	
KW	immunoglobulin G; IgG; Fc region.	
XX		
OS	Chimeric - Homo sapiens.	
XX	Chimeric - Mus sp.	
FH	Key	Location/Qualifiers
FT	Protein	1..22
FT		/label= Signal peptide
FT		/note= "Derived from murine Ig kappa sequence"
FT	Protein	23..302
FT		/label= Mature_human_BCMA_IgG_Fc_fusion_protein
FT	Region	23..75
FT		/note= "Derived from human BCMA protein"
FT	Region	76..302
FT		/note= "Derived from human IgG Fc region"
FT	Domain	24..302
FT		/label= Cysteine rich domain
FT		/note= "Derived from human BCMA"
XX		
XX	WO200124811-A1.	
XX		
PD	12-APR-2001.	
XX		
PF	05-OCT-2000; 2000MO-US27579.	
XX		
XX	06-OCT-1999; 99US-0157933.	
PR	11-FEB-2000; 2000US-018107.	
XX	30-JUN-2000; 2000US-0215688.	
XX		
PA	(BIOJ) BIOGEN INC.	
XX	(APOT-) APOTEC R & D SA.	
PI	Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;	
XX		
DR	WPI; 2001-266242/27.	
XX	N-PDSB; AAD03847.	
PT	Treating a mammal for a condition associated with undesired cell	
PT	proliferation such as cancer or carcinoma, comprises administering a	
PT	composition comprising A Proliferation Inducing Ligand Receptor	
PT	(APRIL-R) antagonist	
XX		
PS	Example 1; Fig 3B; 85pp; English.	
XX		
CC	The invention relates to a method of treating a mammal for a condition	
CC	associated with undesired cell proliferation such as cancer or	
CC	carcinoma. The method involves administering a composition comprising	
CC	A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as the	
CC	B cell maturation protein (BCM or BCMA) antagonist that antagonises the	
CC	interaction between APRIL and its cognate receptor(s). This method is	
CC	useful for treating undesired cell proliferation such as cancer or	
CC	carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,	
CC	prostate carcinoma, and other carcinomas whose proliferation is modulated	
CC	by APRIL. It is also useful for treating autoimmune diseases (Grave's	

CC	disease; systemic lupus erythematosus-SLE); hypertension, cardiovascular disease, renal disorders, B-cell lympho-proliferative disorder, and CC immunosuppressive diseases, organ transplantation, inflammation and CC human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signaling pathway between CC APRIL-R and its ligand APRIL-R DNA is also useful in gene therapy.
CC	The present sequence is a fusion construct containing human APRIL-R CC also referred as BCMA or BCM protein, Fc region of human immunoglobulin G (IgG) and a signal sequence from murine Ig kappa cDNA.
CC	
XX	Sequence 302 AA;
SQ	
OY	Query Match 95.1%; Score 270; DB 22; Length 302; Best Local Similarity 96.0%; Fred. No. 2.ee-24; Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
Dn	1 MAGCSONEYFDSLTHACIPCOLRCSSNTPPLTCORYCNASVTSVKGIN 50 27 MAGCSONEYFDSLTHACIPCOLRCSSNTPPLTCORYCNASVTSVKGV 76
RESULT 12	
ID	AAB60699
XX	AAB60699 standard; Protein; 302 AA.
AC	AAB60699;
DT	22-MAY-2001 (first entry)
DE	Mouse IgG s1gnal/human BAFF-R/human Igg Fc fusion protein, BAFF-R-Fc.
XX	
KM	Human BAFF-R: BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; B-cell maturation inhibitor; lymphoproliferative disorder; hypertension; autoimmune disorder; B-cell lymphoproliferative disorder; HIV infection; renal disorder; immunosuppressive disorder; systemic erythematous; organ transplantatcion; anemia; Granule's disease; multiple myeloma; autoimmune haemolytic anaemia; Leukaemia; rapidly progressive glomerulonephritis; B-cell carcinoma; Leukaemia; rapidly progressive glomerulonephritis; Lymphoma; gene therapy; cancer; tumour; Igg Fc; fusion construct.
KW	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Mus sp.
XX	
PN	WO200112812-A2.
XX	
PD	22-FEB-2001.
XX	
PF	16-AUG-2000; 2000MO-US22507.
XX	
PR	17-AUG-1999; 99US-0149378. 11-FEB-2000; 2000US-0181684. 18-FEB-2000; 2000US-0183536.
PR	
XX	
PA	(BIOL) BIOGEN INC. (APOT-) APOTEC R & D SA.
PA	
PI	Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P; Thompson J;
PI	
XX	
DR	WPI. 2001-202866/20. N-PsDB; AAF59999.
XX	
PT	Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog -
PT	
XX	
XX	Example 4; Fig 2; 59pp; English.
XX	
CC	The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of

CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFF-R fusion protein BAFF-R-FC,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153
 CC of human BAFF-R and a human Igg Fc sequence.

XX SQ Sequence 302 AA;
 Query Match 95.1%; Score 270; DB 22; Length 302;
 Best Local Similarity 96.0%; Pred. No. 2.6e-24;
 Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGTN 50
 DB 27 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGVD 76

RESULT 13

AAE15501

ID AAE15501 standard; peptide; 58 AA.

XX AC AAE15501;

XX DT 12-MAR-2002 (first entry)

XX DE Human B cell maturation protein cysteine rich extracellular region.

XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX OS Homo sapiens.

XX PN WO200187979-A2.

XX PD 22-NOV-2001.

XX PF 14-MAY-2001; 2001WO-US15567.

XX PR 12-MAY-2000; 2000US-204039P.

XX PR 27-JUN-2000; 2000US-214591P.

XX PR 14-MAY-2001; 2001US-0214591.

XX PA (AMGE-) AMGEN INC.

XX PI Theill LE, Yu G;

XX PI WPI; 2002-066686/09.

XX DR Inhibiting activity of B cell maturation protein and/or transmembrane
 XX PT activator and intracellular cyclophilin ligand interactor, by
 XX PT administering a binding partner for APRIL, a tumor necrosis factor

PT family ligand -

PS Disclosure; Fig 13; 94pp; English.

XX CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease (multiple
 CC Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region.

XX SQ Sequence 58 AA;

Query Match 93.0%; Score 264; DB 23; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.3e-24;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGTNA 51

DB 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGTNA 47

RESULT 14

AAB60700

ID AAB60700 standard; Protein; 157 AA.

XX AC AAB60700;

XX DT 22-MAY-2001 (first entry)

XX DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.

XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.

XX OS Homo sapiens.

XX PN WO200112912-A2.

XX PD 22-FEB-2001.

XX PF 16-AUG-2000; 2000WO-US22507.

XX PR 17-AUG-1999; 99US-0149378.

XX PR 11-FEB-2000; 2000US-0181684.

XX PR 18-FEB-2000; 2000US-0183536.

XX PA (BIOJ) BIOGEN INC.

XX PA (APOT-) APOTEC R & D SA.

XX PI Mackay F, Browning J, Ambrose C, Teschopp J, Schneider P;

XX PI Thompson J;

DR WPI: 2001-202866/20.
DR N-PSDB; AAB60000.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAF-R-receptor
XX polypeptide, chimeric molecule comprising receptor or anti-BAF-R
XX antibody homolog

Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAF-R receptor (BAF-R, also known
XX as BCMA) protein, or a BAF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX agent, and also plays a role in the development of hypertension and
XX related disorders. BAF-R, fusion proteins containing it, and BAF-R-
XX specific antibodies can be used for inhibiting B-cell growth, dendritic
XX cell-induced B-cell growth and maturation, and immunoglobulin production,
XX and in the treatment of autoimmune disorders, B-cell lymphoproliferative
XX disorders, hypertension and renal disorders. The BAF-R proteins may also
XX be used in the treatment of immunosuppressive disorders and HIV
XX infection, and in patients undergoing organ transplantation. The BAF-R
XX protein or BAF-R specific antibodies may be used for treating
XX suppressing or altering an immune response involving a signalling pathway
XX between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
XX inhibits B-cell growth and maturation it is useful for treating diseases
XX such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
XX Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
XX progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
XX human BAF-R may be used in gene therapy to treat tumours, lymphomas,
XX autoimmune disorders and inherited B-cell-associated disorders. The
XX present sequence represents a human BAF-R protein sequence as encoded
XX by plasmid pJ57535. However, this BAF-R protein sequence is 27 amino
XX acids shorter than that given in AAB60698.

XX Sequence 157 AA;

Query Match 71.0%; Score 201.5; DB 22; Length 157;
Best Local Similarity 82.4%; Pred. No. 2e-16; Indels 9; Gaps 3;
Matches 42; Conservative 0; Mismatches 0;

OY 1 MAGOSQNEYFDSLHACIPCOLRCSNTPLTCQRYCNASVTNSVKTNA 51
DB 4 MAG---QNEYFDSLHACIPCOLR--NTPLTCQRYCNASVTN---GTNA 45

RESULT 15

AAE15486 standard; peptide: 34 AA.

AAE15486;

12-MAR-2002 (first entry)

Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

Human; transmembrane activator and intracellular CAML interactor; TACI;
cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
rheumatoid arthritis; atherosclerosis.

Homo sapiens.

WO200187979-A2.

22-NOV-2001.

14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.

(AMGE-) AMGEN INC.

Thell LE, Yu G;

WPI: 2002-066666/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand

Claim 1; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
XX family ligand), having the consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein cysteine-rich consensus region.

XX Sequence 34 AA;

Query Match 70.8%; Score 201; DB 23; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.6e-17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

OY 5 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 38
DB 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 34

Search completed: January 7, 2003, 09:37:25
Job time : 19.2782 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:38:19 ; Search time 6.64662 Seconds
(without alignments)
543.836 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGCQNEVFDLSLLHACIP.....LTCQRYCNASVTNSVKGTNA 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/pct NEW COMB.pcp.*
2: /cgn2_6/ptodata/2/paa/US06 NEW COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07 NEW COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US08 NEW COMB.pcp.*
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6: /cgn2_6/ptodata/2/paa/US10 NEW COMB.pcp.*
7: /cgn2_6/ptodata/2/paa/US60 NEW COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	100.0	184	1	PCT-US02-34376-6
2	284	100.0	184	1	PCT-US02-06001-39
3	284	100.0	184	5	US-09-848-271-2
4	284	100.0	184	6	US-10-281-053-6
5	284	100.0	184	6	US-10-087-080-39
6	201	70.8	34	1	PCT-US02-34376-11
7	201	70.8	34	6	US-10-281-053-11
8	70.5	24.8	1548	6	US-10-180-903-2
9	67.5	23.8	166	6	US-10-293-816-6
10	67.5	23.8	293	6	US-10-268-951-22
11	67.5	23.8	293	6	US-10-258-368-1
12	67.5	23.8	293	6	US-10-293-816-2
13	67.5	23.8	301	6	US-10-258-368-12
14	67.5	23.8	334	6	US-10-258-368-8
15	67.5	23.8	366	6	US-10-258-368-6
16	67.5	23.8	404	6	US-10-258-368-15
17	66.5	23.4	33	1	PCT-US02-34376-13
18	66.5	23.4	333	6	US-10-281-053-13
19	63.5	22.4	133	6	US-10-209-582-950
20	60.5	21.3	3034	6	US-10-120-801-70
21	60.5	21.3	3034	6	US-10-150-811-70
22	60.5	21.3	3034	6	US-10-131-409-70
23	60.5	21.3	3034	6	US-10-139-854-70
24	60.5	21.3	3034	6	US-10-150-813-70
25	60.5	21.3	3034	6	US-10-150-164-70
26	59	20.8	34	1	PCT-US02-34376-14

27	59	20.8	34	6	US-10-281-053-14	Sequence 14, Appl
28	59	20.8	87	1	PCT-US02-32727-2251	Sequence 2251, Ap
29	59	20.8	87	6	US-10-057-498-2251	Sequence 2251, Ap
30	59	20.4	162	6	US-10-218-102-420	Sequence 420, App
31	58	20.4	277	5	US-09-724-676-75440	Sequence 75440, A
32	58	20.4	277	5	US-09-724-676A-75440	Sequence 75440, A
33	58	20.4	367	5	US-09-724-676-75441	Sequence 75441, A
34	58	20.4	367	5	US-09-724-676A-75441	Sequence 75441, A
35	58	20.4	1485	5	US-08-724-676-75445	Sequence 75445, A
36	58	20.4	1485	5	US-08-724-676A-75445	Sequence 75445, A
37	58	20.4	1604	5	US-09-724-676-75444	Sequence 75444, A
38	58	20.4	1604	5	US-09-724-676A-75444	Sequence 75444, A
39	58	20.4	1659	5	US-09-724-676-75443	Sequence 75443, A
40	58	20.4	1659	5	US-09-724-676A-75443	Sequence 75443, A
41	58	20.4	1685	5	US-09-724-676-75442	Sequence 75442, A
42	58	20.4	1685	5	US-09-724-676A-75442	Sequence 75442, A
43	58	20.4	1816	6	US-10-299-058-2	Sequence 2, Appli
44	58	20.4	1816	6	US-10-299-058-4	Sequence 4, Appli
45	57	20.1	337	6	US-10-270-333-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1
PCT-US02-34376-6
; Sequence 6, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Zhu, Hong-Ring
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86-PC
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-34376-6

Query Match 100.0%; Score 284; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAGCQNEVFDLSLLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTNA 51
Db 4 MAGCQNEVFDLSLLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTNA 54

RESULT 2
PCT-US02-06001-39
; Sequence 39, Application PC/TUS0206001
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer

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/ FILE REFERENCE: 018501-000840PC
/ CURRENT APPLICATION NUMBER: PCT/US02/06001
/ CURRENT FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: US 60/272,206
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: US 60/281,149
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: US 60/284,555
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
PCT-US02-06001-39

Query Match          100.0%; Score 284; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 51
DB 4 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 54

RESULT 3
/ Sequence 2, Application US/09848271
/ GENERAL INFORMATION:
/ APPLICANT: Ruben, Steven
/ APPLICANT: Baker, Kevin
/ TITLE OF INVENTION: Human Tumor Necrosis Factor TR18 and Methods Based Thereon
/ FILE REFERENCE: PF526
/ CURRENT APPLICATION NUMBER: US/09/848,271
/ CURRENT FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: 60/254,931
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/236,038
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/201,852
/ PRIOR FILING DATE: 2000-05-04
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-848-271-2

Query Match          100.0%; Score 284; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 51
DB 4 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 54

RESULT 4
/ Sequence 6, Application US/10281053
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
/ APPLICANT: Liu, Yingfang
/ APPLICANT: Xu, Liangguo
/ TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
/ TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
/ FILE REFERENCE: 2879-86
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/ CURRENT APPLICATION NUMBER: US/10/281,053
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,106
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 60/348,962
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: 60/354,966
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/403,364
/ PRIOR FILING DATE: 2002-08-13
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-281-053-6

Query Match          100.0%; Score 284; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 51
DB 4 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 54

RESULT 5
/ Sequence 39, Application US/10087080
/ GENERAL INFORMATION:
/ APPLICANT: Mack, David H.
/ APPLICANT: Markowitz, Sanford David
/ APPLICANT: Ros Biotechnology, Inc.
/ TITLE OF INVENTION: Novel Methods of diagnosis of Metastatic Colorectal
/ TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
/ TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
/ FILE REFERENCE: 018501-000840US
/ CURRENT APPLICATION NUMBER: US/10/087,080
/ CURRENT FILING DATE: 2002-10-25
/ PRIOR APPLICATION NUMBER: US 60/272,206
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: US 60/281,149
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: US 60/284,555
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
/ OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match          100.0%; Score 284; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 51
DB 4 MAGCCSNEYFDSLHACIPCOLRGSSNTPPLTCORYCNASVTNSVKGTTA 54

RESULT 6
/ Sequence 11, Application PC/TUS0234376
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
```


APPLICANT: Liu, Yingfang
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
FILE REFERENCE: 2879-86-PCT
CURRENT FILING DATE: 2002-10-24
PCT-US02-34376-11
PCT-US02-34376-11

Query Match 70.8%; Score 201; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.9e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

Qy 5 CSQNEVFDLSLHACIPCOLRCSNTPTLTCQRYC 38
Db 1 CSQNEVFDLSLHACIPCOLRCSNTPTLTCQRYC 34

RESULT 7
US-10-281-053-11
Sequence 11, Application US/10281053
GENERAL INFORMATION:
APPLICANT: Zhang, Hongyi
APPLICANT: Shu, Hongbing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Liangguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
FILE REFERENCE: 2879-86
CURRENT FILING DATE: 2002-10-24
PCT-US02-34376-11
PCT-US02-34376-11

Query Match 70.8%; Score 201; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.9e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

Qy 5 CSQNEVFDLSLHACIPCOLRCSNTPTLTCQRYC 38
Db 1 CSQNEVFDLSLHACIPCOLRCSNTPTLTCQRYC 34

RESULT 8
US-10-180-903-2
Sequence 2, Application US/10180903

GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
FILE REFERENCE: R-720
CURRENT FILING DATE: 2002-06-25
PCT-US02-34376-11
PCT-US02-34376-11

Query Match 24.8%; Score 70.5; DB 6; Length 1548;
Best Local Similarity 34.7%; Pred. No. 3.4; Indels 5; Gaps 1;
Matches 17; Conservative 5; Mismatches 22

Qy 4 QCSQNEVFDLSLHACIPCOLRCSNTPTLTCQRYC 47
Db 1151 ECNAVEYWDGSHRCQPCCHKRCSCGPFSDQCYCTCPRETFLLNTTCVK 1199

RESULT 9
US-10-293-816-6
Sequence 6, Application US/10293816
GENERAL INFORMATION:
APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
FILE REFERENCE: 44158/254623
CURRENT FILING DATE: 2002-11-12
PCT-US02-34376-11
PCT-US02-34376-11

Query Match 23.8%; Score 67.5; DB 6; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.5; Indels 15; Gaps 1;
Matches 11; Conservative 9; Mismatches 15

Qy 5 CSQNEVFDLSLHACIPCOLRCSNTPTLTCQRYC 40
Db 34 CPSEQYWDPLLTGTCMCKTICNHQS-QRTCAAFCS 68

RESULT 10
US-10-268-951-22
Sequence 22, Application US/10268951
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P2
CURRENT FILING DATE: 2002-10-11
PCT-US02-34376-11
PCT-US02-34376-11

Qy 5 CSQNEVFDLSLHACIPCOLRCSNTPTLTCQRYC 40
Db 34 CPSEQYWDPLLTGTCMCKTICNHQS-QRTCAAFCS 68

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; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22
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Query Match 23.8%; Score 67.5; DB 6; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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QY 5 CSQNEYFDSLHACIPQALRCSSNTPLTCORYCNA 40
Db 34 CPEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 68
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RESULT 11
US-10-258-368-1
; Sequence 1, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; TITLE OF INVENTION: Tacti As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-1
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Query Match 23.8%; Score 67.5; DB 6; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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QY 5 CSQNEYFDSLHACIPQALRCSSNTPLTCORYCNA 40
Db 34 CPEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 68
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RESULT 12
US-10-293-816-2
; Sequence 2, Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Brem, Richard J.
; APPLICANT: Von Bulow, Gotz
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```
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2
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Query Match 23.8%; Score 67.5; DB 6; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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QY 5 CSQNEYFDSLHACIPQALRCSSNTPLTCORYCNA 40
Db 34 CPEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 68
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RESULT 13
US-10-258-368-12
; Sequence 12, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; TITLE OF INVENTION: Tacti As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 12
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-12
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Query Match 23.8%; Score 67.5; DB 6; Length 301;
Best Local Similarity 30.6%; Pred. No. 2.3;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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QY 5 CSQNEYFDSLHACIPQALRCSSNTPLTCORYCNA 40
Db 42 CPEQYWDPLGTGCMSCKTICNHQS-QRTCAAFCRS 76
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RESULT 14
US-10-258-368-8
; Sequence 8, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; TITLE OF INVENTION: Tacti As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
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